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## APPLICATION TRANSMITTAL LETTER

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(Typed or Printed Name of Person Mailing Paper or Fee)

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(Signature of Person Mailing Paper or Fee)

Transmitted herewith for filing is the patent application of Patricia A. BILLING-MEDEL, Maurice COHEN, Tracey L. COLPITTS, Paula N. FRIEDMAN, Edward N. GRANADOS, Steven C. HODGES, Michael R. KLASS, Jon D. KRATOCHVIL, Lisa ROBERTS-RAPP, John C. RUSSELL and Stephen D. STROUPE for REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF THE URINARY TRACT, which is a continuation-in-part of U.S. application serial no. 08/856,652, filed May 15, 1997.

Enclosed are:

- 6 sheet(s) of X formal \_\_\_ informal drawing(s).  
\_\_\_ A claim for foreign priority under 35 U.S.C. § 119/363 in \_\_\_ a separate document \_\_\_ the declaration.  
\_\_\_ A claim for priority under 35 U.S.C. § 119(e)(1) in \_\_\_ a separate document \_\_\_ the declaration.  
\_\_\_ A certified copy of the priority document.  
\_\_\_ Verified Statement(s) Claiming Small Entity Status.  
X Other: Sequence Listing in paper form (pp. 86-95); Sequence Listing in computer readable form; and Statement to Support Filing and Submission in Accordance with 37 C.F.R. §§ 1.821-1.825.

The declaration of the inventor X is enclosed X unsigned.

The fee has been calculated as follows:

A. Basic Application Fee		\$790.00
B. Total Claims 21 - 20 = 1	x \$22.00	22.00
C. Independent Claims 8 - 3 = 5	x \$82.00	410.00
D. If multiple dependent claims present, add	\$270.00	0.00
E. Total Application Fee (Total of A, B, C, & D)	=	1222.00
F. If verified statement of small entity status is enclosed, reduce Total Application Fee by 50%		NA
G. Application Fee Due (E - F)	=	1222.00
H. Assignment Recording Fee of \$40.00 if assignment document is enclosed	\$40.00	NA
I. TOTAL FEE (G + H)		\$1222.00

Respectfully submitted,

Date: MAY 15, 1998

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### Cross-Reference to Related Application

## Background of the Invention

15 This invention relates generally to detecting diseases of the urinary tract. Furthermore, the invention also relates to reagents and methods for detecting diseases of the urinary tract. More particularly, the present invention relates to reagents such as polynucleotide sequences and the polypeptide sequences encoded thereby, as well as methods which utilize these sequences. The polynucleotide and polypeptide sequences  
20 are useful for detecting, diagnosing, staging, monitoring, prognosticating, in vivo imaging, preventing or treating, or determining predisposition to diseases or conditions of the urinary tract such as urinary tract cancers.

The organs of the urinary tract include the bladder, kidneys, and ureter. The incidence of urinary tract cancers in the United States is projected to be 86,300 cases diagnosed and 24,700 related deaths to occur during 1998. The most prevalent of the urinary tract cancers is bladder cancer, with projections of 54,400 new cases diagnosed and 12,500 related deaths to occur during 1998 (American Cancer Society statistics).

Procedures used for detecting, diagnosing, staging, monitoring, prognosticating, in vivo imaging, preventing or treating, or determining predisposition to diseases or conditions of the urinary tract such as urinary tract cancers are of critical importance to the outcome of the patient. For example, patients diagnosed with localized bladder cancer have a greater than a 90% five-year survival rate as compared to a survival rate of 50%, and less than 10%, for patients diagnosed with regionally extended and distally metastasized bladder cancers, respectively (American Cancer Society statistics). Currently, the best initial indication of early bladder cancer is the presence of microscopic hematuria which, if detected, may lead to the invasive and costly procedures of cystoscopy and cytology, procedures that are necessary for a

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definitive diagnosis. Hematuria as a marker for bladder cancer is poor; less than 10% of patients with this symptom are eventually diagnosed with bladder cancer. Thus, use of hematuria as a marker for bladder cancer results in many unnecessary cystoscopic and cytological procedures. C. McNeil, J. National Cancer Institute 23, 1704-1705  
5 (1996). In addition, 20% of bladder cancer cases are negative for hematuria. D.L. Lamm, et al., CA Cancer J. Clin. 46: 93-112 (1996).

Bladder cancer patients are closely monitored by cystoscopy to detect persistent or recurrent disease or to detect early distant metastasis because recurrence rates following initial treatment are high (50-80%). W.R. Fair, et al., In: Cancer: Principles  
10 and Practice of Oncology, Fourth Edition, pp. 1052-1072, Philadelphia, PA: J.B. Lippincott Co. 1993. This procedure is performed every three months for at least five years. C. McNeil, supra. In addition, cytology, another mainstay of bladder cancer monitoring, is unreliable in detecting superficial, grade 1 tumors. G.M. Farrow, J. Occupational Med. 32: 817-821 (1990). Alternative methods that are sensitive for  
15 detecting bladder cancer and/or its recurrence and which are less expensive and/or invasive, therefore, are needed.

A critical step in managing patients with urinary tract cancer is the presurgical staging of the cancer to provide prognostic value and criteria for designing optimal therapy. For example, clinical and pathological staging of bladder cancer can disagree  
20 in more than 50% of patients with respect to the extent of invasion by a primary tumor. W.R. Fair, supra. Therefore, clinical staging of urinary tract cancers could be improved by utilizing new markers found in serum or urine which could differentiate between different stages of muscle invasion. Such markers could be mRNA or protein markers expressed by cells originating from the primary tumor but residing in blood,  
25 bone marrow or lymph nodes, and could serve as sensitive indicators for metastasis to these distal organs. For example, bladder cells have been detected in the bone marrow of patients with bladder cancer using immunohistochemical techniques, thus suggesting the occurrence of metastasis to the bone. K. Pantel, et al., Onkologie 18: 394-401 (1995).

Such procedures also could include assays based upon the appearance of  
30 various disease markers in test samples such as blood, plasma, serum or urine obtained by minimally invasive procedures which are detectable by immunological methods. These procedures would provide information to aid the physician in managing the patient with disease of the urinary tract at a low cost to the patient. Markers such as  
35 prostate specific antigen (PSA) and human chorionic gonadotropin (hCG) exist and are used clinically for screening patients for prostate cancer and testicular cancer, respectively. For example, PSA normally is secreted by the prostate at high levels into

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the seminal fluid, but is present in very low levels in the blood of men with normal prostates. Elevated levels of PSA protein in serum are used in the early detection of prostate cancer or disease in asymptomatic men. See, for example, G.E. Hanks, et al., In: Cancer: Principles and Practice of Oncology, Vol. 1, Fourth Edition, pp. 1073-1113, Philadelphia, PA: J.B. Lippincott Co. 1993. M. K. Schwartz, et al., In: Cancer: Principles and Practice of Oncology, Vol. 1, Fourth Edition, pp. 531-542, Philadelphia, PA: J.B. Lippincott Co. 1993. Likewise, the management of urinary tract diseases could be improved by the use of new markers normally expressed in an organ of the urinary tract but found in elevated amounts in an inappropriate body compartment as a result of the disease of the urinary tract.

Further, new markers which could predict the biologic behavior of early urinary tract cancers would also be of significant value. Early urinary tract cancers that threaten or will threaten the life of the patient are more clinically important than those that do not or will not be a threat. G.E. Hanks, supra. A need therefore exists for new markers which can differentiate between the clinically important and unimportant urinary tract cancers. Such markers would allow the clinician to accurately identify and effectively treat early cancers localized to the urinary tract which could otherwise metastasize and kill the patient. For example, the detection by immunoassay of a protein marker appearing in urine prior to or concomitant with bladder cancer recurrence would be useful. NMP22 and BTA are two protein markers found in urine which currently are being evaluated for utility as monitoring markers. C. McNeil, supra. Preliminary results with these markers suggest that a different marker with greater sensitivity and/or specificity would provide further improvement for the accurate detection of bladder cancer.

It therefore would be advantageous to provide specific methods and reagents for the early detecting, diagnosing, staging, monitoring, prognosticating, in vivo imaging, preventing or treating, or determining predisposition to diseases and conditions associated with the urinary tract. Such methods would include assaying a test sample for products of a gene which are overexpressed in diseases and conditions associated with the urinary tract including cancer. Such methods may also include assaying a test sample for products of a gene which have been altered in the disease or condition associated with the urinary tract. Such methods may further include assaying a test sample for products of a gene whose distribution among the various tissues and compartments of the body have been altered by a urinary tract-associated disease or condition including cancer. Such methods would comprise making cDNA from mRNA in the test sample, amplifying, when necessary, portions of the cDNA corresponding to the gene or a fragment thereof, and detecting the cDNA product as an

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Figure 1: Schematic representation of the experimental design. The figure shows a vertical timeline of events. At the top, 'Pre-Test' is indicated. Below it, 'Training' is shown with a box labeled 'Training' and a note '10 days'. This is followed by 'Test' with a box labeled 'Test' and a note '10 days'. The timeline ends with 'Post-Test'. The timeline is divided into three sections: 'Pre-Test', 'Training', and 'Test'. The 'Training' section is further divided into 'Training' and 'Test' sub-sections. The 'Test' section is further divided into 'Test' and 'Post-Test' sub-sections. The timeline is labeled with 'Time' on the left and 'Days' on the right.

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Figure 1: Schematic representation of the experimental design. The figure shows a vertical timeline of events. At the top, 'Pre-Test' is indicated. Below it, 'Training' is shown with a box labeled 'Training' and a note '100% correct'. This is followed by 'Test' with a box labeled 'Test' and a note '100% correct'. Then, 'Transfer' is shown with a box labeled 'Transfer' and a note '100% correct'. Finally, 'Post-Test' is indicated at the bottom. The timeline is marked with 'Time' on the left and 'Performance' on the right. The 'Performance' axis shows a high level of performance during Training and Test, a drop during Transfer, and a recovery during Post-Test. The 'Time' axis shows the sequence of events: Pre-Test, Training, Test, Transfer, and Post-Test.

Figure 1: Schematic representation of the experimental design. The figure shows a vertical timeline of events. At the top, 'Pre-Test' is indicated. Below it, 'Training' is shown with a box labeled 'Training' and a note '100% correct'. This is followed by 'Test' with a box labeled 'Test' and a note '100% correct'. Then, 'Transfer' is shown with a box labeled 'Transfer' and a note '100% correct'. Finally, 'Post-Test' is indicated at the bottom. The timeline is marked with 'Time' on the left and 'Performance' on the right. The 'Performance' axis shows a high level of performance during Training and Test, a drop during Transfer, and a recovery during Post-Test. The 'Time' axis shows the sequence of events: Pre-Test, Training, Test, Transfer, and Post-Test.

50% identity with a sequence selected from the group consisting of SEQUENCE ID NOS 1-12, and fragments or complements thereof. Amplification can be performed by the polymerase chain reaction. Also, the test sample can be reacted with a solid phase prior to performing the method, prior to amplification or prior to detection. This  
5 reaction can be a direct or an indirect reaction. Further, the detection step can comprise utilizing a detectable label capable of generating a measurable signal. The detectable label can be attached to a solid phase.

The present invention further provides a method of detecting a target UT116 polynucleotide in a test sample suspected of containing target UT116 polynucleotides,  
10 which comprises (a) contacting the test sample with at least one UT116 oligonucleotide as a sense primer and at least one UT116 oligonucleotide as an anti-sense primer, and amplifying same to obtain a first stage reaction product; (b) contacting the first stage reaction product with at least one other UT116 oligonucleotide to obtain a second stage reaction product, with the proviso that the other UT116 oligonucleotide is located 3' to  
15 the UT116 oligonucleotides utilized in step (a) and is complementary to the first stage reaction product; and (c) detecting the second stage reaction product as an indication of the presence of a target UT116 polynucleotide in the test sample. The UT116 oligonucleotides selected as reagents in the method have at least 50% identity with a sequence selected from the group consisting of SEQUENCE ID NOS 1-12, and  
20 fragments or complements thereof. Amplification may be performed by the polymerase chain reaction. The test sample can be reacted either directly or indirectly with a solid phase prior to performing the method, or prior to amplification, or prior to detection. The detection step also comprises utilizing a detectable label capable of generating a measurable signal; further, the detectable label can be attached to a solid phase. Test  
25 kits useful for detecting target UT116 polynucleotides in a test sample are also provided which comprise a container containing at least one UT116-specific polynucleotide selected from the group consisting of SEQUENCE ID NOS 1-12, and fragments or complements thereof. These test kits further comprise containers with tools useful for collecting test samples (such as, for example, blood, urine, saliva and stool). Such  
30 tools include lancets and absorbent paper or cloth for collecting and stabilizing blood; swabs for collecting and stabilizing saliva; and cups for collecting and stabilizing urine or stool samples. Collection materials, such as papers, cloths, swabs, cups, and the like, may optionally be treated to avoid denaturation or irreversible adsorption of the sample. The collection materials also may be treated with or contain preservatives,  
35 stabilizers or antimicrobial agents to help maintain the integrity of the specimens.

The present invention also provides a purified polynucleotide or fragment thereof derived from a UT116 gene. The purified polynucleotide is capable of

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selectively hybridizing to the nucleic acid of the UT116 gene, or a complement thereof. The polynucleotide has at least 50% identity with a polynucleotide selected from the group consisting of SEQUENCE ID NOS 1-12, and fragments or complements thereof. Further, the purified polynucleotide can be produced by recombinant and/or  
5 synthetic techniques. The purified recombinant polynucleotide can be contained within a recombinant vector. The invention further comprises a host cell transfected with the recombinant vector.

The present invention further provides a recombinant expression system comprising a nucleic acid sequence that includes an open reading frame derived from  
10 UT116. The nucleic acid sequence has at least 50% identity with a sequence selected from the group consisting of SEQUENCE ID NOS 1-12, and fragments or complements thereof. The nucleic acid sequence is operably linked to a control sequence compatible with a desired host. Also provided is a cell transfected with this recombinant expression system.

The present invention also provides a polypeptide encoded by UT116. The polypeptide can be produced by recombinant technology, provided in purified form, or produced by synthetic techniques. The polypeptide comprises an amino acid sequence which has at least 50% identity with an amino acid sequence selected from the group consisting of SEQUENCE ID NO 25, SEQUENCE ID NO 26, SEQUENCE ID NO  
15 27, SEQUENCE ID NO 28 and SEQUENCE ID NO 29, and fragments thereof.

Also provided is an antibody which specifically binds to at least one UT116 epitope. The antibody can be a polyclonal or monoclonal antibody. The epitope is derived from an amino acid sequence selected from the group consisting of SEQUENCE ID NO 25, SEQUENCE ID NO 26, SEQUENCE ID NO 27,  
20 SEQUENCE ID NO 28 and SEQUENCE ID NO 29, and fragments thereof. Assay kits for determining the presence of UT116 antigen or anti-UT116 antibody in a test sample are also included. In one embodiment, the assay kits comprise a container containing at least one UT116 polypeptide having at least 50% identity with an amino acid sequence selected from the group consisting of SEQUENCE ID NO 25,  
25 SEQUENCE ID NO 26, SEQUENCE ID NO 27, SEQUENCE ID NO 28 and SEQUENCE ID NO 29, and fragments thereof. Further, the test kit can comprise a container with tools useful for collecting test samples (such as blood, urine, saliva, and stool). Such tools include lancets and absorbent paper or cloth for collecting and stabilizing blood; swabs for collecting and stabilizing saliva; and cups for collecting and  
30 stabilizing urine or stool samples. Collection materials, such as papers, cloths, swabs, cups, and the like, may optionally be treated to avoid denaturation or irreversible adsorption of the sample. These collection materials also may be treated with or  
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contain preservatives, stabilizers or antimicrobial agents to help maintain the integrity of the specimens. Also, the polypeptide can be attached to a solid phase.

In another embodiment of the invention, antibodies or fragments thereof against the UT116 antigen can be used to detect or image localization of the antigen in a patient for the purpose of detecting or diagnosing a disease or condition. Such antibodies can be polyclonal or monoclonal, or made by molecular biology techniques; and can be labeled with a variety of detectable labels, including, but not limited to, radioisotopes and paramagnetic metals. Furthermore, antibodies or fragments thereof, whether monoclonal, polyclonal, or made by molecular biology techniques, can be used as therapeutic agents for the treatment of diseases characterized by expression of the UT116 antigen. In the case of therapeutic applications, the antibody may be used without derivitization, or it may be derivitized with a cytotoxic agent such as a radioisotope, enzyme, toxin, drug, prodrug, or the like.

Another assay kit for determining the presence of UT116 antigen or anti-UT116 antibody in a test sample comprises a container containing an antibody which specifically binds to a UT116 antigen, wherein the UT116 antigen comprises at least one UT116-encoded epitope. The UT116 antigen has at least about 60% sequence similarity to a sequence of a UT116-encoded antigen selected from the group consisting of SEQUENCE ID NO 25, SEQUENCE ID NO 26, SEQUENCE ID NO 27, SEQUENCE ID NO 28 and SEQUENCE ID NO 29, and fragments thereof. These test kits can further comprise containers with tools useful for collecting test samples (such as blood, urine, saliva, and stool). Such tools include lancets and absorbent paper or cloth for collecting and stabilizing blood; swabs for collecting and stabilizing saliva; cups for collecting and stabilizing urine or stool samples. Collection materials, papers, cloths, swabs, cups and the like, may optionally be treated to avoid denaturation or irreversible adsorption of the sample. These collection materials also may be treated with, or contain, preservatives, stabilizers or antimicrobial agents to help maintain the integrity of the specimens. The antibody can be attached to a solid phase.

A method for producing a polypeptide which contains at least one epitope of UT116 is provided, which method comprises incubating host cells transfected with an expression vector. This vector comprises a polynucleotide sequence encoding a polypeptide, wherein the polypeptide comprises an amino acid sequence having at least 50% identity with a UT116 amino acid sequence selected from the group consisting of SEQUENCE ID NO 25, SEQUENCE ID NO 26, SEQUENCE ID NO 27, SEQUENCE ID NO 28 and SEQUENCE ID NO 29, and fragments thereof.

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A method for detecting UT116 antigen in a test sample suspected of containing UT116 antigen also is provided. The method comprises contacting the test sample with an antibody or fragment thereof which specifically binds to at least one epitope of a UT116 antigen, for a time and under conditions sufficient for the formation of  
5 antibody/antigen complexes; and detecting the presence of such complexes containing the antibody as an indication of the presence of UT116 antigen in the test sample. The antibody can be attached to a solid phase and may be either a monoclonal or polyclonal antibody. Furthermore, the antibody specifically binds to at least one UT116 antigen selected from the group consisting of SEQUENCE ID NO 25, SEQUENCE ID NO 26,  
10 SEQUENCE ID NO 27, SEQUENCE ID NO 28 and SEQUENCE ID NO 29, and fragments thereof.

Another method is provided which detects antibodies which specifically bind to UT116 antigen in a test sample suspected of containing these antibodies. The method comprises contacting the test sample with a polypeptide which contains at least one  
15 UT116 epitope, wherein the UT116 epitope comprises an amino acid sequence having at least 50% identity with an amino acid sequence encoded by a UT116 polynucleotide, or a fragment thereof. Contacting is carried out for a time and under conditions sufficient to allow antigen/antibody complexes to form. The method further entails detecting complexes which contain the polypeptide. The polypeptide can be attached to  
20 a solid phase. Further, the polypeptide can be a recombinant protein or a synthetic peptide having at least 50% identity with an amino acid sequence selected from the group consisting of SEQUENCE ID NO 25, SEQUENCE ID NO 26, SEQUENCE ID NO 27, SEQUENCE ID NO 28 and SEQUENCE ID NO 29, and fragments thereof.

The present invention provides a cell transfected with a UT116 nucleic acid  
25 sequence that encodes at least one epitope of a UT116 antigen, or fragment thereof. The nucleic acid sequence is selected from the group consisting of SEQUENCE ID NOS 1-12, and fragments or complements thereof.

A method for producing antibodies to UT116 antigen also is provided, which method comprises administering to an individual an isolated immunogenic polypeptide  
30 or fragment thereof, wherein the isolated immunogenic polypeptide comprises at least one UT116 epitope. The immunogenic polypeptide is administered in an amount sufficient to produce an immune response. The isolated, immunogenic polypeptide comprises an amino acid sequence selected from the group consisting of SEQUENCE ID NO 25, SEQUENCE ID NO 26, SEQUENCE ID NO 27, SEQUENCE ID NO 28  
35 and SEQUENCE ID NO 29, and fragments thereof.

Another method for producing antibodies which specifically bind to UT116 antigen is disclosed, which method comprises administering to an individual a plasmid

comprising a nucleic acid sequence which encodes at least one UT116 epitope derived from an amino acid sequence selected from the group consisting of SEQUENCE ID NO 25, SEQUENCE ID NO 26, SEQUENCE ID NO 27, SEQUENCE ID NO 28 and SEQUENCE ID NO 29, and fragments thereof. The plasmid is administered in an amount such that the plasmid is taken up by cells in the individual and expressed at levels sufficient to produce an immune response.

Also provided is a composition of matter that comprises a UT116 polynucleotide of at least about 10-12 nucleotides having at least 50% identity with a polynucleotide selected from the group consisting of SEQUENCE ID NOS 1-12, and fragments or complements thereof. The UT116 polynucleotide encodes an amino acid sequence having at least one UT116 epitope. Another composition of matter provided by the present invention comprises a polypeptide with at least one UT116 epitope of about 8-10 amino acids. The polypeptide comprises an amino acid sequence having at least 50% identity with an amino acid sequence selected from the group consisting of SEQUENCE ID NO 25, SEQUENCE ID NO 26, SEQUENCE ID NO 27, SEQUENCE ID NO 28 and SEQUENCE ID NO 29, and fragments thereof. Also provided is a gene, or fragment thereof, coding for a UT116 polypeptide which has at least 50% identity to SEQUENCE ID NO 25; and a gene, or a fragment thereof, comprising DNA having at least 50% identity with SEQUENCE ID NO 11 or SEQUENCE ID NO 12.

#### Brief Description of the Drawings

Figures 1A-1C show the nucleotide alignment of clones 3353644 (SEQUENCE ID NO 1), 2804743 (SEQUENCE ID NO 2), 1891065 (SEQUENCE ID NO 3), 1543671 (SEQUENCE ID NO 4), 1863905 (SEQUENCE ID NO 5), 1314679 (SEQUENCE ID NO 6), 1901337 (SEQUENCE ID NO 7), 1900086 (SEQUENCE ID NO 8), 2325070 (SEQUENCE ID NO 9), 3969672 (SEQUENCE ID NO 10), the full-length sequence of clone 1543671 (designated as clone 1543671IH (SEQUENCE ID NO 11)), and the consensus sequence (SEQUENCE ID NO 12) derived therefrom.

Figure 2 shows the contig map depicting the formation of the consensus nucleotide sequence (SEQUENCE ID NO 12) from the nucleotide alignment of overlapping clones 3353644 (SEQUENCE ID NO 1), 2804743 (SEQUENCE ID NO 2), 1891065 (SEQUENCE ID NO 3), 1543671 (SEQUENCE ID NO 4), 1863905 (SEQUENCE ID NO 5), 1314679 (SEQUENCE ID NO 6), 1901337 (SEQUENCE ID NO 7), 1900086 (SEQUENCE ID NO 8), 2325070 (SEQUENCE ID NO 9), 3969672 (SEQUENCE ID NO 10), and 1543671IH (SEQUENCE ID NO 11).

Figure 3 is a scan of an ethidium bromide-stained agarose gel of RNA from tissue extracts of normal bladder and bladder cancers with the corresponding Northern blot of RNA using a UT116-specific radiolabeled probe.

Figure 4 shows the results of the Western blot performed on a panel of tissue  
5 extracts using antiserum against the synthetic UT116 peptide of SEQUENCE ID NO 27.

#### Detailed Description of the Invention

The present invention provides a gene, or a fragment thereof, which codes for a  
10 UT116 polypeptide having at least about 50% identity to SEQUENCE ID NO 25. The present invention further encompasses a UT116 gene, or a fragment thereof, comprising DNA which has at least about 50% identity with SEQUENCE ID NO 11 or SEQUENCE ID NO 12.

The present invention also provides methods for assaying a test sample for  
15 products of a urinary tract tissue gene designated as UT116, which comprises making cDNA from mRNA in the test sample, and detecting the cDNA as an indication of the presence of urinary tract tissue gene UT116. The method may include an amplification step, wherein one or more portions of the mRNA from UT116 corresponding to the gene or fragments thereof, is amplified. Methods also are provided for assaying for the  
20 translation products of UT116. Test samples which may be assayed by the methods provided herein include tissues, cells, body fluids and secretions. The present invention also provides reagents such as oligonucleotide primers and polypeptides which are useful in performing these methods.

Portions of the nucleic acid sequences disclosed herein are useful as primers for  
25 the reverse transcription of RNA or for the amplification of cDNA; or as probes to determine the presence of certain mRNA sequences in test samples. Also disclosed are nucleic acid sequences which permit the production of encoded polypeptide sequences which are useful as standards or reagents in diagnostic immunoassays, as targets for pharmaceutical screening assays and/or as components or as target sites for various  
30 therapies. Monoclonal and polyclonal antibodies directed against at least one epitope contained within these polypeptide sequences are useful as delivery agents for therapeutic agents as well as for diagnostic tests and for screening for diseases or conditions associated with UT116, especially urinary tract cancer. Isolation of sequences of other portions of the gene of interest can be accomplished utilizing probes  
35 or PCR primers derived from these nucleic acid sequences. This allows additional probes of the mRNA or cDNA of interest to be established, as well as corresponding encoded polypeptide sequences. These additional molecules are useful in detecting,

diagnosing, staging, monitoring, prognosticating, in vivo imaging, preventing or treating, or determining the predisposition to diseases and conditions of the urinary tract, such as urinary tract cancer, characterized by UT116, as disclosed herein.

Techniques for determining amino acid sequence "similarity" are well-known in the art. In general, "similarity" means the exact amino acid to amino acid comparison of two or more polypeptides at the appropriate place, where amino acids are identical or possess similar chemical and/or physical properties such as charge or hydrophobicity. A so-termed "percent similarity" then can be determined between the compared polypeptide sequences. Techniques for determining nucleic acid and amino acid sequence identity also are well known in the art and include determining the nucleotide sequence of the mRNA for that gene (usually via a cDNA intermediate) and determining the amino acid sequence encoded thereby, and comparing this to a second amino acid sequence. In general, "identity" refers to an exact nucleotide to nucleotide or amino acid to amino acid correspondence of two polynucleotides or polypeptide sequences, respectively. Two or more polynucleotide sequences can be compared by determining their "percent identity." Two or more amino acid sequences likewise can be compared by determining their "percent identity." The programs available in the Wisconsin Sequence Analysis Package, Version 8 (available from Genetics Computer Group, Madison, WI), for example, the GAP program, are capable of calculating both the identity between two polynucleotides and the identity and similarity between two polypeptide sequences, respectively. Other programs for calculating identity or similarity between sequences are known in the art.

The compositions and methods described herein will enable the identification of certain markers as indicative of a urinary tract tissue disease or condition; the information obtained therefrom will aid in the detecting, diagnosing, staging, monitoring, prognosticating, in vivo imaging, preventing or treating, or determining diseases or conditions associated with UT116, especially urinary tract cancer. Test methods include, for example, probe assays which utilize the sequence(s) provided herein and which also may utilize nucleic acid amplification methods such as the polymerase chain reaction (PCR), the ligase chain reaction (LCR), and hybridization. In addition, the nucleotide sequences provided herein contain open reading frames from which an immunogenic epitope may be found. This epitope is believed to be unique to the disease state or condition associated with UT116. It also is thought that the polynucleotides or polypeptides and protein encoded by the UT116 gene are useful as a marker. This marker is either elevated in disease such as urinary tract cancer, altered in disease such as urinary tract cancer, or present as a normal protein but appearing in an inappropriate body compartment. The uniqueness of the epitope may be determined by

(i) its immunological reactivity and specificity with antibodies directed against proteins and polypeptides encoded by the UT116 gene, and (ii) its nonreactivity with any other tissue markers. Methods for determining immunological reactivity are well-known and include, but are not limited to, for example, radioimmunoassay (RIA), enzyme-linked immunoabsorbent assay (ELISA), hemagglutination (HA), fluorescence polarization immunoassay (FPIA), chemiluminescent immunoassay (CLIA) and others. Several examples of suitable methods are described herein.

Unless otherwise stated, the following terms shall have the following meanings:

10 A polynucleotide "derived from" or "specific for" a designated sequence refers to a polynucleotide sequence which comprises a contiguous sequence of approximately at least about 6 nucleotides, preferably at least about 8 nucleotides, more preferably at least about 10-12 nucleotides, and even more preferably at least about 15-20 nucleotides corresponding, i.e., identical or complementary to, a region of the  
15 designated nucleotide sequence. The sequence may be complementary or identical to a sequence which is unique to a particular polynucleotide sequence as determined by techniques known in the art. Comparisons to sequences in databanks, for example, can be used as a method to determine the uniqueness of a designated sequence. Regions from which sequences may be derived, include but are not limited to, regions  
20 encoding specific epitopes, as well as non-translated and/or non-transcribed regions.

The derived polynucleotide will not necessarily be derived physically from the nucleotide sequence of interest under study, but may be generated in any manner, including, but not limited to, chemical synthesis, replication, reverse transcription or transcription, which is based on the information provided by the sequence of bases in  
25 the region(s) from which the polynucleotide is derived. As such, it may represent either a sense or an antisense orientation of the original polynucleotide. In addition, combinations of regions corresponding to that of the designated sequence may be modified in ways known in the art to be consistent with the intended use.

A "fragment" of a specified polynucleotide refers to a polynucleotide sequence  
30 which comprises a contiguous sequence of approximately at least about 6 nucleotides, preferably at least about 8 nucleotides, more preferably at least about 10-12 nucleotides, and even more preferably at least about 15-20 nucleotides corresponding, i.e., identical or complementary to, a region of the specified nucleotide sequence.

The term "primer" denotes a specific oligonucleotide sequence which is  
35 complementary to a target nucleotide sequence and used to hybridize to the target nucleotide sequence. A primer serves as an initiation point for nucleotide

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polymerization catalyzed by either DNA polymerase, RNA polymerase or reverse transcriptase.

The term "probe" denotes a defined nucleic acid segment (or nucleotide analog segment, e.g., PNA as defined hereinbelow) which can be used to identify a specific polynucleotide present in samples bearing the complementary sequence.

"Encoded by" refers to a nucleic acid sequence which codes for a polypeptide sequence, wherein the polypeptide sequence or a portion thereof contains an amino acid sequence of at least 3 to 5 amino acids, more preferably at least 8 to 10 amino acids, and even more preferably at least 15 to 20 amino acids from a polypeptide encoded by the nucleic acid sequence. Also encompassed are polypeptide sequences which are immunologically identifiable with a polypeptide encoded by the sequence. Thus, a "polypeptide," "protein," or "amino acid" sequence has at least about 50% identity, preferably about 60% identity, more preferably about 75-85% identity, and most preferably about 90-95% or more identity to a UT116 amino acid sequence. Further, the UT116 "polypeptide," "protein," or "amino acid" sequence may have at least about 60% similarity, preferably at least about 75% similarity, more preferably about 85% similarity, and most preferably about 95% or more similarity to a polypeptide or amino acid sequence of UT116. This amino acid sequence can be selected from the group consisting of SEQUENCE ID NO 25, SEQUENCE ID NO 26, SEQUENCE ID NO 27, SEQUENCE ID NO 28 and SEQUENCE ID NO 29, and fragments thereof.

A "recombinant polypeptide," "recombinant protein," or "a polypeptide produced by recombinant techniques," which terms may be used interchangeably herein, describes a polypeptide which by virtue of its origin or manipulation is not associated with all or a portion of the polypeptide with which it is associated in nature and/or is linked to a polypeptide other than that to which it is linked in nature. A recombinant or encoded polypeptide or protein is not necessarily translated from a designated nucleic acid sequence. It also may be generated in any manner, including chemical synthesis or expression of a recombinant expression system.

The term "synthetic peptide" as used herein means a polymeric form of amino acids of any length, which may be chemically synthesized by methods well-known to the routineer. These synthetic peptides are useful in various applications.

The term "polynucleotide" as used herein means a polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides. This term refers only to the primary structure of the molecule. Thus, the term includes double- and single-stranded DNA, as well as double- and single-stranded RNA. It also includes modifications, such as methylation or capping and unmodified forms of the

polynucleotide. The terms “polynucleotide,” “oligomer,” “oligonucleotide,” and “oligo” are used interchangeably herein.

“A sequence corresponding to a cDNA” means that the sequence contains a polynucleotide sequence that is identical or complementary to a sequence in the designated DNA. The degree (or “percent”) of identity or complementarity to the cDNA will be approximately 50% or greater, preferably at least about 70% or greater, and more preferably at least about 90% or greater. The sequence that corresponds to the identified cDNA will be at least about 50 nucleotides in length, preferably at least about 60 nucleotides in length, and more preferably at least about 70 nucleotides in length. The correspondence between the gene or gene fragment of interest and the cDNA can be determined by methods known in the art and include, for example, a direct comparison of the sequenced material with the cDNAs described, or hybridization and digestion with single strand nucleases, followed by size determination of the digested fragments.

“Purified polynucleotide” refers to a polynucleotide of interest or fragment thereof which is essentially free, e.g., contains less than about 50%, preferably less than about 70%, and more preferably less than about 90%, of the protein with which the polynucleotide is naturally associated. Techniques for purifying polynucleotides of interest are well-known in the art and include, for example, disruption of the cell containing the polynucleotide with a chaotropic agent and separation of the polynucleotide(s) and proteins by ion-exchange chromatography, affinity chromatography and sedimentation according to density.

“Purified polypeptide” or “purified protein” means a polypeptide of interest or fragment thereof which is essentially free of, e.g., contains less than about 50%, preferably less than about 70%, and more preferably less than about 90%, cellular components with which the polypeptide of interest is naturally associated. Methods for purifying polypeptides of interest are known in the art.

The term “isolated” means that the material is removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or DNA or polypeptide, which is separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotide could be part of a vector and/or such polynucleotide or polypeptide could be part of a composition, and still be isolated in that the vector or composition is not part of its natural environment.

“Polypeptide” and “protein” are used interchangeably herein and indicate at least one molecular chain of amino acids linked through covalent and/or non-covalent bonds.



1 The terms do not refer to a specific length of the product. Thus peptides, oligopeptides  
and proteins are included within the definition of polypeptide. The terms include post-  
translational modifications of the polypeptide, for example, glycosylations,  
acetylations, phosphorylations and the like. In addition, protein fragments, analogs,  
5 mutated or variant proteins, fusion proteins and the like are included within the  
meaning of polypeptide.

A “fragment” of a specified polypeptide refers to an amino acid sequence which  
comprises at least about 3-5 amino acids, more preferably at least about 8-10 amino  
acids, and even more preferably at least about 15-20 amino acids derived from the  
10 specified polypeptide.

“Recombinant host cells,” “host cells,” “cells,” “cell lines,” “cell cultures,” and  
other such terms denoting microorganisms or higher eukaryotic cell lines cultured as  
unicellular entities refer to cells which can be, or have been, used as recipients for  
recombinant vector or other transferred DNA, and include the original progeny of the  
15 original cell which has been transfected.

As used herein “replicon” means any genetic element, such as a plasmid, a  
chromosome or a virus, that behaves as an autonomous unit of polynucleotide  
replication within a cell.

A “vector” is a replicon in which another polynucleotide segment is attached,  
20 such as to bring about the replication and/or expression of the attached segment.

The term “control sequence” refers to a polynucleotide sequence which is  
necessary to effect the expression of a coding sequence to which it is ligated. The  
nature of such control sequences differs depending upon the host organism. In  
prokaryotes, such control sequences generally include a promoter, a ribosomal binding  
25 site and terminators; in eukaryotes, such control sequences generally include  
promoters, terminators and, in some instances, enhancers. The term “control  
sequence” thus is intended to include at a minimum all components whose presence is  
necessary for expression, and also may include additional components whose presence  
is advantageous, for example, leader sequences.

30 “Operably linked” refers to a situation wherein the components described are in  
a relationship permitting them to function in their intended manner. Thus, for example,  
a control sequence “operably linked” to a coding sequence is ligated in such a manner  
that expression of the coding sequence is achieved under conditions compatible with  
the control sequence.

35 The term “open reading frame” or “ORF” refers to a region of a polynucleotide  
sequence which encodes a polypeptide. This region may represent a portion of a  
coding sequence or a total coding sequence.

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A "coding sequence" is a polynucleotide sequence which is transcribed into mRNA and translated into a polypeptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a translation start codon at the 5' -terminus and a translation stop codon at the 3' -terminus. A coding sequence can include, but is not limited to, mRNA, cDNA and recombinant polynucleotide sequences.

The term "immunologically identifiable with/as" refers to the presence of epitope(s) and polypeptide(s) which also are present in and are unique to the designated polypeptide(s). Immunological identity may be determined by antibody binding and/or competition in binding. These techniques are known to the routineer and also are described herein. The uniqueness of an epitope also can be determined by computer searches of known data banks, such as GenBank, for the polynucleotide sequence which encodes the epitope and by amino acid sequence comparisons with other known proteins.

As used herein, "epitope" means an antigenic determinant of a polypeptide or protein. Conceivably, an epitope can comprise three amino acids in a spatial conformation which is unique to the epitope. Generally, an epitope consists of at least five such amino acids and more usually, it consists of at least eight to ten amino acids. Methods of examining spatial conformation are known in the art and include, for example, x-ray crystallography and two-dimensional nuclear magnetic resonance.

A "conformational epitope" is an epitope that is comprised of a specific juxtaposition of amino acids in an immunologically recognizable structure, such amino acids being present on the same polypeptide in a contiguous or non-contiguous order or present on different polypeptides.

A polypeptide is "immunologically reactive" with an antibody when it binds to an antibody due to antibody recognition of a specific epitope contained within the polypeptide. Immunological reactivity may be determined by antibody binding, more particularly, by the kinetics of antibody binding, and/or by competition in binding using as competitor(s) a known polypeptide(s) containing an epitope against which the antibody is directed. The methods for determining whether a polypeptide is immunologically reactive with an antibody are known in the art.

As used herein, the term "immunogenic polypeptide containing an epitope of interest" means naturally occurring polypeptides of interest or fragments thereof, as well as polypeptides prepared by other means, for example, by chemical synthesis or the expression of the polypeptide in a recombinant organism.

The term "transfection" refers to the introduction of an exogenous polynucleotide into a prokaryotic or eucaryotic host cell, irrespective of the method

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used for the introduction. The term “transfection” refers to both stable and transient introduction of the polynucleotide, and encompasses direct uptake of polynucleotides, transformation, transduction, and f-mating. Once introduced into the host cell, the exogenous polynucleotide may be maintained as a non-integrated replicon, for example, a plasmid, or alternatively, may be integrated into the host genome.

“Treatment” refers to prophylaxis and/or therapy.

The term “individual” as used herein refers to vertebrates, particularly members of the mammalian species and includes, but is not limited to, domestic animals, sports animals, primates and humans; more particularly, the term refers to humans.

The term “sense strand” or “plus strand” (or “+”) as used herein denotes a nucleic acid that contains the sequence that encodes the polypeptide. The term “antisense strand” or “minus strand” (or “-”) denotes a nucleic acid that contains a sequence that is complementary to that of the “plus” strand.

The term “test sample” refers to a component of an individual’s body which is the source of the analyte (such as antibodies of interest or antigens of interest). These components are well known in the art. A test sample is typically anything suspected of containing a target sequence. Test samples can be prepared using methodologies well known in the art such as by obtaining a specimen from an individual and, if necessary, disrupting any cells contained thereby to release target nucleic acids. These test samples include biological samples which can be tested by the methods of the present invention described herein and include human and animal body fluids such as whole blood, serum, plasma, cerebrospinal fluid, sputum, bronchial washing, bronchial aspirates, urine, lymph fluids, and various external secretions of the respiratory, intestinal and genitourinary tracts, tears, saliva, milk, white blood cells, myelomas and the like; biological fluids such as cell culture supernatants; tissue specimens which may be fixed; and cell specimens which may be fixed.

“Purified product” refers to a preparation of the product which has been isolated from the cellular constituents with which the product is normally associated and from other types of cells which may be present in the sample of interest.

“PNA” denotes a “peptide nucleic acid analog” which may be utilized in a procedure such as an assay described herein to determine the presence of a target. “MA” denotes a “morpholino analog” which may be utilized in a procedure such as an assay described herein to determine the presence of a target. See, for example, U.S. Patent No. 5,378,841, which is incorporated herein by reference. PNAs are neutrally charged moieties which can be directed against RNA targets or DNA. PNA probes used in assays in place of, for example, the DNA probes of the present invention, offer advantages not achievable when DNA probes are used. These advantages include

manufacturability, large scale labeling, reproducibility, stability, insensitivity to changes in ionic strength and resistance to enzymatic degradation which is present in methods utilizing DNA or RNA. These PNAs can be labeled with ("attached to") such signal generating compounds as fluorescein, radionucleotides, chemiluminescent compounds and the like. PNAs or other nucleic acid analogs such as MAs thus can be used in assay methods in place of DNA or RNA. Although assays are described herein utilizing DNA probes, it is within the scope of the routineer that PNAs or MAs can be substituted for RNA or DNA with appropriate changes if and as needed in assay reagents.

10            "Analyte," as used herein, is the substance to be detected which may be present in the test sample. The analyte can be any substance for which there exists a naturally occurring specific binding member (such as an antibody), or for which a specific binding member can be prepared. Thus, an analyte is a substance that can bind to one or more specific binding members in an assay. "Analyte" also includes any antigenic substances, haptens, antibodies and combinations thereof. As a member of a specific binding pair, the analyte can be detected by means of naturally occurring specific binding partners (pairs) such as the use of intrinsic factor protein as a member of a specific binding pair for the determination of Vitamin B12, the use of folate-binding protein to determine folic acid, or the use of a lectin as a member of a specific binding pair for the determination of a carbohydrate. The analyte can include a protein, a polypeptide, an amino acid, a nucleotide target and the like. The analyte can be soluble in a body fluid such as blood, blood plasma or serum, urine or the like. The analyte can be in a tissue, either on a cell surface or within a cell. The analyte can be on or in a cell dispersed in a body fluid such as blood, urine, breast aspirate, or obtained as a biopsy sample.

The terms "diseases of the urinary tract," "urinary tract disease," and "condition of the urinary tract " are used interchangeably herein to refer to any disease or condition of the urinary tract including, but not limited to, cystitis, interstitial cystitis, urethritis, nephrosclerosis, nephritis, and cancer.

30            "Urinary tract cancer," as used herein, refers to any malignant disease of the urinary tract including but not limited to, adenocarcinoma, transitional cell carcinoma, squamous cell carcinoma, carcinoma in situ, clear carcinoma, granular cell carcinoma and sarcomatoid carcinoma.

An "Expressed Sequence Tag" or "EST" refers to the partial sequence of a cDNA insert which has been made by reverse transcription of mRNA extracted from a tissue followed by insertion into a vector.

A “transcript image” refers to a table or list giving the quantitative distribution of ESTs in a library and represents the genes active in the tissue from which the library was made.

The present invention provides assays which utilize specific binding members.

- 5 A “specific binding member,” as used herein, is a member of a specific binding pair. That is, two different molecules where one of the molecules, through chemical or physical means, specifically binds to the second molecule. Therefore, in addition to antigen and antibody specific binding pairs of common immunoassays, other specific binding pairs can include biotin and avidin, carbohydrates and lectins, complementary  
10 nucleotide sequences, effector and receptor molecules, cofactors and enzymes, enzyme inhibitors, and enzymes and the like. Furthermore, specific binding pairs can include members that are analogs of the original specific binding members, for example, an analyte-analog. Immunoreactive specific binding members include antigens, antigen fragments, antibodies and antibody fragments, both monoclonal and polyclonal and  
15 complexes thereof, including those formed by recombinant DNA molecules.

The term “hapten,” as used herein, refers to a partial antigen or non-protein binding member which is capable of binding to an antibody, but which is not capable of eliciting antibody formation unless coupled to a carrier protein.

- A “capture reagent,” as used herein, refers to an unlabeled specific binding  
20 member which is specific either for the analyte as in a sandwich assay, for the indicator reagent or analyte as in a competitive assay, or for an ancillary specific binding member, which itself is specific for the analyte, as in an indirect assay. The capture reagent can be directly or indirectly bound to a solid phase material before the performance of the assay or during the performance of the assay, thereby enabling the  
25 separation of immobilized complexes from the test sample.

- The “indicator reagent” comprises a “signal-generating compound” (“label”) which is capable of generating and generates a measurable signal detectable by external means, conjugated (“attached”) to a specific binding member. In addition to being an antibody member of a specific binding pair, the indicator reagent also can be a member  
30 of any specific binding pair, including either hapten-anti-hapten systems such as biotin or anti-biotin, avidin or biotin, a carbohydrate or a lectin, a complementary nucleotide sequence, an effector or a receptor molecule, an enzyme cofactor and an enzyme, an enzyme inhibitor or an enzyme and the like. An immunoreactive specific binding member can be an antibody, an antigen, or an antibody/antigen complex that is capable  
35 of binding either to the polypeptide of interest as in a sandwich assay, to the capture reagent as in a competitive assay, or to the ancillary specific binding member as in an indirect assay. When describing probes and probe assays, the term “reporter molecule”

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may be used. A reporter molecule comprises a signal generating compound as described hereinabove conjugated to a specific binding member of a specific binding pair, such as carbazole or adamantane.

The various “signal-generating compounds” (labels) contemplated include chromagens, catalysts such as enzymes, luminescent compounds such as fluorescein and rhodamine, chemiluminescent compounds such as dioxetanes, acridiniums, phenanthridiniums and luminol, radioactive elements and direct visual labels. Examples of enzymes include alkaline phosphatase, horseradish peroxidase, beta-galactosidase and the like. The selection of a particular label is not critical, but it must be capable of producing a signal either by itself or in conjunction with one or more additional substances.

“Solid phases” (“solid supports”) are known to those in the art and include the walls of wells of a reaction tray, test tubes, polystyrene beads, magnetic or non-magnetic beads, nitrocellulose strips, membranes, microparticles such as latex particles, sheep (or other animal) red blood cells and Duracytes® (red blood cells “fixed” by pyruvic aldehyde and formaldehyde, available from Abbott Laboratories, Abbott Park, IL) and others. The “solid phase” is not critical and can be selected by one skilled in the art. Thus, latex particles, microparticles, magnetic or non-magnetic beads, membranes, plastic tubes, walls of microtiter wells, glass or silicon chips, sheep (or other suitable animal’s) red blood cells and Duracytes® are all suitable examples. Suitable methods for immobilizing peptides on solid phases include ionic, hydrophobic, covalent interactions and the like. A “solid phase,” as used herein, refers to any material which is insoluble, or can be made insoluble by a subsequent reaction. The solid phase can be chosen for its intrinsic ability to attract and immobilize the capture reagent. Alternatively, the solid phase can retain an additional receptor which has the ability to attract and immobilize the capture reagent. The additional receptor can include a charged substance that is oppositely charged with respect to the capture reagent itself or to a charged substance conjugated to the capture reagent. As yet another alternative, the receptor molecule can be any specific binding member which is immobilized upon (attached to) the solid phase and which has the ability to immobilize the capture reagent through a specific binding reaction. The receptor molecule enables the indirect binding of the capture reagent to a solid phase material before the performance of the assay or during the performance of the assay. The solid phase thus can be a plastic, derivatized plastic, magnetic or non-magnetic metal, glass or silicon surface of a test tube, microtiter well, sheet, bead, microparticle, chip, sheep (or other suitable animal’s) red blood cells, Duracytes® and other configurations known to those of ordinary skill in the art.

It is contemplated and within the scope of the present invention that the solid phase also can comprise any suitable porous material with sufficient porosity to allow access by detection antibodies and a suitable surface affinity to bind antigens.

5 Microporous structures generally are preferred, but materials with a gel structure in the hydrated state may be used as well. Such useful solid supports include, but are not limited to, nitrocellulose and nylon. It is contemplated that such porous solid supports described herein preferably are in the form of sheets of thickness from about 0.01 to 0.5 mm, preferably about 0.1 mm. The pore size may vary within wide limits and preferably is from about 0.025 to 15 microns, especially from about 0.15 to 15  
10 microns. The surface of such supports may be activated by chemical processes which cause covalent linkage of the antigen or antibody to the support. The irreversible binding of the antigen or antibody is obtained, however, in general, by adsorption on the porous material by poorly understood hydrophobic forces. Other suitable solid supports are known in the art.

15 Reagents.

The present invention provides reagents such as polynucleotide sequences derived from a urinary tract tissue of interest and designated as UT116, polypeptides encoded thereby and antibodies specific for these polypeptides. The present invention also provides reagents such as oligonucleotide fragments derived from the disclosed  
20 polynucleotides and nucleic acid sequences complementary to these polynucleotides. The polynucleotides, polypeptides, or antibodies of the present invention may be used to provide information leading to the detecting, diagnosing, staging, monitoring, prognosticating, in vivo imaging, preventing or treating of, or determining the predisposition to, diseases and conditions of the urinary tract, such as urinary tract  
25 cancer. The sequences disclosed herein represent unique polynucleotides which can be used in assays or for producing a specific profile of gene transcription activity. Such assays are disclosed in European Patent Number 0373203B1 and International Publication No. WO 95/11995, which are hereby incorporated by reference.

Selected UT116-derived polynucleotides can be used in the methods described  
30 herein for the detection of normal or altered gene expression. Such methods may employ UT116 polynucleotides or oligonucleotides, fragments or derivatives thereof, or nucleic acid sequences complementary thereto.

The polynucleotides disclosed herein, their complementary sequences, or fragments of either, can be used in assays to detect, amplify or quantify genes, nucleic  
35 acids, cDNAs or mRNAs relating to urinary tract tissue disease and conditions associated therewith. They also can be used to identify an entire or partial coding region of a UT116 polypeptide. They further can be provided in individual containers

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in the form of a kit for assays, or provided as individual compositions. If provided in a kit for assays, other suitable reagents such as buffers, conjugates and the like may be included.

5 The polynucleotide may be in the form of RNA or DNA. Polynucleotides in the form of DNA, cDNA, genomic DNA, nucleic acid analogs and synthetic DNA are within the scope of the present invention. The DNA may be double-stranded or single-stranded, and if single stranded, may be the coding (sense) strand or non-coding (anti-sense) strand. The coding sequence which encodes the polypeptide may be identical to the coding sequence provided herein or may be a different coding sequence which  
10 coding sequence, as a result of the redundancy or degeneracy of the genetic code, encodes the same polypeptide as the DNA provided herein.

This polynucleotide may include only the coding sequence for the polypeptide, or the coding sequence for the polypeptide and an additional coding sequence such as a leader or secretory sequence or a proprotein sequence, or the coding sequence for the  
15 polypeptide (and optionally an additional coding sequence) and non-coding sequence, such as a non-coding sequence 5' and/or 3' of the coding sequence for the polypeptide.

In addition, the invention includes variant polynucleotides containing modifications such as polynucleotide deletions, substitutions or additions; and any polypeptide modification resulting from the variant polynucleotide sequence. A  
20 polynucleotide of the present invention also may have a coding sequence which is a naturally occurring allelic variant of the coding sequence provided herein.

In addition, the coding sequence for the polypeptide may be fused in the same reading frame to a polynucleotide sequence which aids in expression and secretion of a polypeptide from a host cell, for example, a leader sequence which functions as a  
25 secretory sequence for controlling transport of a polypeptide from the cell. The polypeptide having a leader sequence is a preprotein and may have the leader sequence cleaved by the host cell to form the polypeptide. The polynucleotides may also encode for a proprotein which is the protein plus additional 5' amino acid residues. A protein having a prosequence is a proprotein and may, in some cases, be an inactive form of  
30 the protein. Once the prosequence is cleaved, an active protein remains. Thus, the polynucleotide of the present invention may encode for a protein, or for a protein having a prosequence, or for a protein having both a presequence (leader sequence) and a prosequence.

The polynucleotides of the present invention may also have the coding sequence  
35 fused in frame to a marker sequence which allows for purification of the polypeptide of the present invention. The marker sequence may be a hexa-histidine tag supplied by a pQE-9 vector to provide for purification of the polypeptide fused to the marker in the

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case of a bacterial host, or, for example, the marker sequence may be a hemagglutinin (HA) tag when a mammalian host, e.g. a COS-7 cell line, is used. The HA tag corresponds to an epitope derived from the influenza hemagglutinin protein. See, for example, I. Wilson et al., Cell 37:767 (1984).

5           It is contemplated that polynucleotides will be considered to hybridize to the sequences provided herein if there is at least 50%, preferably at least 70%, and more preferably at least 90% identity between the polynucleotide and the sequence.

          The present invention also provides an antibody produced by using a purified  
10   UT116 polypeptide of which at least a portion of the polypeptide is encoded by a UT116 polynucleotide selected from the polynucleotides provided herein. These antibodies may be used in the methods provided herein for the detection of UT116 antigen in test samples. The presence of UT116 antigen in the test samples is indicative of the presence of a urinary tract disease or condition. The antibody also may be used for therapeutic purposes, for example, in neutralizing the activity of UT116 polypeptide  
15   in conditions associated with altered or abnormal expression.

          The present invention further relates to a UT116 polypeptide which has the deduced amino acid sequence as provided herein, as well as fragments, analogs and derivatives of such polypeptide. The polypeptide of the present invention may be a recombinant polypeptide, a natural purified polypeptide or a synthetic polypeptide. The  
20   fragment, derivative or analog of the UT116 polypeptide may be one in which one or more of the amino acid residues is substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code; or it may be one in which one or more of the amino acid residues includes a substituent group; or it  
25   may be one in which the polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol); or it may be one in which the additional amino acids are fused to the polypeptide, such as a leader or secretory sequence or a sequence which is employed for purification of the polypeptide or a proprotein sequence. Such fragments,  
30   derivatives and analogs are within the scope of the present invention. The polypeptides and polynucleotides of the present invention are provided preferably in an isolated form and preferably purified.

          Thus, a polypeptide of the present invention may have an amino acid sequence that is identical to that of the naturally occurring polypeptide or that is different by  
35   minor variations due to one or more amino acid substitutions. The variation may be a "conservative change" typically in the range of about 1 to 5 amino acids, wherein the substituted amino acid has similar structural or chemical properties, e.g., replacement

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of leucine with isoleucine or threonine with serine. In contrast, variations may include nonconservative changes, e.g., replacement of a glycine with a tryptophan. Similar minor variations may also include amino acid deletions or insertions, or both.

Guidance in determining which and how many amino acid residues may be substituted, inserted or deleted without changing biological or immunological activity may be found using computer programs well known in the art, for example, DNASTAR software (DNASTAR Inc., Madison WI).

Probes constructed according to the polynucleotide sequences of the present invention can be used in various assay methods to provide various types of analysis. For example, such probes can be used in fluorescent in situ hybridization (FISH) technology to perform chromosomal analysis, and used to identify cancer-specific structural alterations in the chromosomes, such as deletions or translocations that are visible from chromosome spreads or detectable using PCR-generated and/or allele specific oligonucleotides probes, allele specific amplification or by direct sequencing. Probes also can be labeled with radioisotopes, directly- or indirectly- detectable haptens, or fluorescent molecules, and utilized for in situ hybridization studies to evaluate the mRNA expression of the gene comprising the polynucleotide in tissue specimens or cells.

This invention also provides teachings as to the production of the polynucleotides and polypeptides provided herein.

#### Probe Assays

The sequences provided herein may be used to produce probes which can be used in assays for the detection of nucleic acids in test samples. The probes may be designed from conserved nucleotide regions of the polynucleotides of interest or from non-conserved nucleotide regions of the polynucleotide of interest. The design of such probes for optimization in assays is within the skill of the routineer. Generally, nucleic acid probes are developed from non-conserved or unique regions when maximum specificity is desired, and nucleic acid probes are developed from conserved regions when assaying for nucleotide regions that are closely related to, for example, different members of a multi-gene family or in related species like mouse and man.

The polymerase chain reaction (PCR) is a technique for amplifying a desired nucleic acid sequence (target) contained in a nucleic acid or mixture thereof. In PCR, a pair of primers are employed in excess to hybridize to the complementary strands of the target nucleic acid. The primers are each extended by a polymerase using the target nucleic acid as a template. The extension products become target sequences themselves, following dissociation from the original target strand. New primers then are hybridized and extended by a polymerase, and the cycle is repeated to geometrically

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increase the number of target sequence molecules. PCR is disclosed in U.S. Patents 4,683,195 and 4,683,202, which are incorporated herein by reference.

5 The Ligase Chain Reaction (LCR) is an alternate method for nucleic acid amplification. In LCR, probe pairs are used which include two primary (first and second) and two secondary (third and fourth) probes, all of which are employed in molar excess to target. The first probe hybridizes to a first segment of the target strand, and the second probe hybridizes to a second segment of the target strand, the first and second segments being contiguous so that the primary probes abut one another in 5'phosphate-3'hydroxyl relationship, and so that a ligase can covalently fuse or ligate the two probes into a fused product. In addition, a third (secondary) probe can hybridize to a portion of the first probe and a fourth (secondary) probe can hybridize to a portion of the second probe in a similar abutting fashion. Of course, if the target is initially double stranded, the secondary probes also will hybridize to the target complement in the first instance. Once the ligated strand of primary probes is separated from the target strand, it will hybridize with the third and fourth probes which can be ligated to form a complementary, secondary ligated product. It is important to realize that the ligated products are functionally equivalent to either the target or its complement. By repeated cycles of hybridization and ligation, amplification of the target sequence is achieved. This technique is described more completely in EP-A- 320 308 to K. Backman published June 16, 1989 and EP-A-439 182 to K. Backman et al, published July 31, 1991, both of which are incorporated herein by reference.

For amplification of mRNAs, it is within the scope of the present invention to reverse transcribe mRNA into cDNA followed by polymerase chain reaction (RT-PCR); or, to use a single enzyme for both steps as described in U.S. Patent No. 25 5,322,770, which is incorporated herein by reference; or reverse transcribe mRNA into cDNA followed by asymmetric gap ligase chain reaction (RT-AGLCR) as described by R.L. Marshall et al., PCR Methods and Applications 4: 80-84 (1994), which also is incorporated herein by reference.

Other known amplification methods which can be utilized herein include but are not limited to the so-called "NASBA" or "3SR" technique described by J.C. Guatelli et al., PNAS USA 87:1874-1878 (1990) and also described by J. Compton, Nature 350 (No. 6313):91-92 (1991); Q-beta amplification as described in published European Patent Application (EPA) No. 4544610; strand displacement amplification (as described in G.T. Walker et al., Clin. Chem. 42:9-13 [1996]) and European Patent Application No. 684315; and target mediated amplification, as described in International Publication No. WO 93/22461.

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Detection of UT116 may be accomplished using any suitable detection method, including those detection methods which are currently well known in the art, as well as detection strategies which may evolve later. Examples of the foregoing presently known detection methods are hereby incorporated herein by reference. See, for  
5 example, Caskey et al., U.S. Patent No. 5,582,989, Gelfand et al., U.S. Patent No. 5,210,015. Examples of such detection methods include target amplification methods as well as signal amplification technologies. An example of presently known detection methods would include the nucleic acid amplification technologies referred to as PCR, LCR, NASBA, SDA, RCR and TMA. See, for example, Caskey et al., U.S. Patent  
10 No. 5,582,989, Gelfand et al., U.S. Patent No. 5,210,015. All of the foregoing are hereby incorporated by reference. Detection may also be accomplished using signal amplification such as that disclosed in Snitman et al., U.S. Patent No. 5,273,882. While the amplification of target or signal is preferred at present, it is contemplated and within the scope of the present invention that ultrasensitive detection methods which do  
15 not require amplification can be utilized herein.

Detection, both amplified and non-amplified, may be (combined) carried out using a variety of heterogeneous and homogeneous detection formats. Examples of heterogeneous detection formats are disclosed in Snitman et al., U.S. Patent No. 5,273,882, Albarella et al in EP-84114441.9, Urdea et al., U.S. Patent No.  
20 5,124,246, Ullman et al. U.S. Patent No. 5,185,243 and Kourilsky et al., U.S. Patent No. 4,581,333. All of the foregoing are hereby incorporated by reference. Examples of homogeneous detection formats are disclosed in, Caskey et al., U.S. Patent No. 5,582,989, Gelfand et al., U.S. Patent No. 5,210,015, which are incorporated herein by reference. Also contemplated and within the scope of the present invention is the  
25 use of multiple probes in the hybridization assay, which use improves sensitivity and amplification of the UT116 signal. See, for example, Caskey et al., U.S. Patent No. 5,582,989, Gelfand et al., U.S. Patent No. 5,210,015, which are incorporated herein by reference.

In one embodiment, the present invention generally comprises the steps of  
30 contacting a test sample suspected of containing a target polynucleotide sequence with amplification reaction reagents comprising an amplification primer, and a detection probe that can hybridize with an internal region of the amplicon sequences. Probes and primers employed according to the method provided herein are labeled with capture and detection labels, wherein probes are labeled with one type of label and primers are  
35 labeled with another type of label. Additionally, the primers and probes are selected such that the probe sequence has a lower melt temperature than the primer sequences. The amplification reagents, detection reagents and test sample are placed under

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modification thereof is employed in the preferred method, the entire target sequence is usually known. Typically, the target sequence is a nucleic acid sequence such as, for example, RNA or DNA.

5 The method provided herein can be used in well-known amplification reactions that include thermal cycle reaction mixtures, particularly in PCR and gap LCR (GLCR). Amplification reactions typically employ primers to repeatedly generate copies of a target nucleic acid sequence, which target sequence is usually a small region of a much larger nucleic acid sequence. Primers are themselves nucleic acid sequences that are complementary to regions of a target sequence. Under amplification  
10 conditions, these primers hybridize or bind to the complementary regions of the target sequence. Copies of the target sequence typically are generated by the process of primer extension and/or ligation which utilizes enzymes with polymerase or ligase activity, separately or in combination, to add nucleotides to the hybridized primers and/or ligate adjacent probe pairs. The nucleotides that are added to the primers or  
15 probes, as monomers or preformed oligomers, are also complementary to the target sequence. Once the primers or probes have been sufficiently extended and/or ligated, they are separated from the target sequence, for example, by heating the reaction mixture to a "melt temperature" which is one in which complementary nucleic acid strands dissociate. Thus, a sequence complementary to the target sequence is formed.  
20 A new amplification cycle then can take place to further amplify the number of target sequences by separating any double stranded sequences, allowing primers or probes to hybridize to their respective targets, extending and/or ligating the hybridized primers or probes and re-separating. The complementary sequences that are generated by amplification cycles can serve as templates for primer extension or filling the gap of  
25 two probes to further amplify the number of target sequences. Typically, a reaction mixture is cycled between 20 and 100 times, more typically, a reaction mixture is cycled between 25 and 50 times. The numbers of cycles can be determined by the routineer. In this manner, multiple copies of the target sequence and its complementary sequence are produced. Thus, primers initiate amplification of the target sequence  
30 when it is present under amplification conditions.

Generally, two primers which are complementary to a portion of a target strand and its complement are employed in PCR. For LCR, four probes, two of which are complementary to a target sequence and two of which are similarly complementary to the target's complement, are generally employed. In addition to the primer sets and  
35 enzymes previously mentioned, a nucleic acid amplification reaction mixture may also comprise other reagents which are well known and include but are not limited to: enzyme cofactors such as manganese; magnesium; salts; nicotinamide adenine

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dinucleotide (NAD); and deoxynucleotide triphosphates (dNTPs) such as, for example, deoxyadenine triphosphate, deoxyguanine triphosphate, deoxycytosine triphosphate and deoxythymine triphosphate.

While the amplification primers initiate amplification of the target sequence, the detection (or hybridization) probe is not involved in amplification. Detection probes are generally nucleic acid sequences or uncharged nucleic acid analogs such as, for example, peptide nucleic acids which are disclosed in International Publication No. WO 92/20702; morpholino analogs which are described in U.S. Patents Nos 5,185,444, 5,034,506 and 5,142,047; and the like. Depending upon the type of label carried by the probe, the probe is employed to capture or detect the amplicon generated by the amplification reaction. The probe is not involved in amplification of the target sequence and therefore may have to be rendered "non-extendible" in that additional dNTPs cannot be added to the probe. In and of themselves, analogs usually are non-extendible and nucleic acid probes can be rendered non-extendible by modifying the 3' end of the probe such that the hydroxyl group is no longer capable of participating in elongation. For example, the 3' end of the probe can be functionalized with the capture or detection label to thereby consume or otherwise block the hydroxyl group. Alternatively, the 3' hydroxyl group simply can be cleaved, replaced or modified. U.S. Patent Application Serial No. 07/049,061 filed April 19, 1993 and incorporated herein by reference describes modifications which can be used to render a probe non-extendible.

The ratio of primers to probes is not important. Thus, either the probes or primers can be added to the reaction mixture in excess whereby the concentration of one would be greater than the concentration of the other. Alternatively, primers and probes can be employed in equivalent concentrations. Preferably, however, the primers are added to the reaction mixture in excess of the probes. Thus, primer to probe ratios of, for example, 5:1 and 20:1, are preferred.

While the length of the primers and probes can vary, the probe sequences are selected such that they have a lower melt temperature than the primer sequences. Hence, the primer sequences are generally longer than the probe sequences. Typically, the primer sequences are in the range of between 20 and 50 nucleotides long, more typically in the range of between 20 and 30 nucleotides long. The typical probe is in the range of between 10 and 25 nucleotides long.

Various methods for synthesizing primers and probes are well known in the art. Similarly, methods for attaching labels to primers or probes are also well known in the art. For example, it is a matter of routine to synthesize desired nucleic acid primers or probes using conventional nucleotide phosphoramidite chemistry and instruments available from Applied Biosystems, Inc., (Foster City, CA), DuPont (Wilmington,

DE), or Milligen (Bedford MA). Many methods have been described for labeling oligonucleotides such as the primers or probes of the present invention. Enzo Biochemical (New York, NY) and Clontech (Palo Alto, CA) both have described and commercialized probe labeling techniques. For example, a primary amine can be attached to a 3' oligo terminus using 3'-Amine-ON CPG™ (Clontech, Palo Alto, CA). Similarly, a primary amine can be attached to a 5' oligo terminus using Aminomodifier II® (Clontech). The amines can be reacted to various haptens using conventional activation and linking chemistries. In addition, copending applications U.S. Serial Nos. 625,566, filed December 11, 1990 and 630,908, filed December 20, 1990, which are each incorporated herein by reference, teach methods for labeling probes at their 5' and 3' termini, respectively. International Publication Nos WO 92/10505, published 25 June 1992, and WO 92/11388, published 9 July 1992, teach methods for labeling probes at their 5' and 3' ends, respectively. According to one known method for labeling an oligonucleotide, a label-phosphoramidite reagent is prepared and used to add the label to the oligonucleotide during its synthesis. See, for example, N.T. Thuong et al., *Tet. Letters* 29(46):5905-5908 (1988); or J.S. Cohen et al., published U.S. Patent Application 07/246,688 (NTIS ORDER No. PAT-APPL-7-246,688) (1989). Preferably, probes are labeled at their 3' and 5' ends.

A capture label is attached to the primers or probes and can be a specific binding member which forms a binding pair with the solid phase reagent's specific binding member. It will be understood that the primer or probe itself may serve as the capture label. For example, in the case where a solid phase reagent's binding member is a nucleic acid sequence, it may be selected such that it binds a complementary portion of the primer or probe to thereby immobilize the primer or probe to the solid phase. In cases where the probe itself serves as the binding member, those skilled in the art will recognize that the probe will contain a sequence or "tail" that is not complementary to the single stranded amplicon members. In the case where the primer itself serves as the capture label, at least a portion of the primer will be free to hybridize with a nucleic acid on a solid phase because the probe is selected such that it is not fully complementary to the primer sequence.

Generally, probe/single stranded amplicon member complexes can be detected using techniques commonly employed to perform heterogeneous immunoassays. Preferably, in this embodiment, detection is performed according to the protocols used by the commercially available Abbott LCx® instrumentation (Abbott Laboratories, Abbott Park, IL).



The primers and probes disclosed herein are useful in typical PCR assays, wherein the test sample is contacted with a pair of primers, amplification is performed, the hybridization probe is added, and detection is performed.

Another method provided by the present invention comprises contacting a test sample with a plurality of polynucleotides, wherein at least one polynucleotide is a UT116 molecule as described herein, hybridizing the test sample with the plurality of polynucleotides and detecting hybridization complexes. Hybridization complexes are identified and quantitated to compile a profile which is indicative of urinary tract tissue disease, such as urinary tract cancer. Expressed RNA sequences may further be detected by reverse transcription and amplification of the DNA product by procedures well-known in the art, including polymerase chain reaction (PCR).

Drug Screening and Gene Therapy.

The present invention also encompasses the use of gene therapy methods for the introduction of anti-sense UT116 derived molecules, such as polynucleotides or oligonucleotides of the present invention, into patients with conditions associated with abnormal expression of polynucleotides related to a urinary tract tissue disease or condition especially urinary tract cancer. These molecules, including antisense RNA and DNA fragments and ribozymes, are designed to inhibit the translation of UT116 mRNA, and may be used therapeutically in the treatment of conditions associated with altered or abnormal expression of UT116 polynucleotide.

Alternatively, the oligonucleotides described above can be delivered to cells by procedures known in the art such that the anti-sense RNA or DNA may be expressed in vivo to inhibit production of a UT116 polypeptide in the manner described above. Antisense constructs to a UT116 polynucleotide, therefore, reverse the action of UT116 transcripts and may be used for treating urinary tract tissue disease conditions, such as urinary tract cancer. These antisense constructs may also be used to treat tumor metastases.

The present invention also provides a method of screening a plurality of compounds for specific binding to UT116 polypeptide(s), or any fragment thereof, to identify at least one compound which specifically binds the UT116 polypeptide. Such a method comprises the steps of providing at least one compound; combining the UT116 polypeptide with each compound under suitable conditions for a time sufficient to allow binding; and detecting the UT116 polypeptide binding to each compound.

The polypeptide or peptide fragment employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of screening utilizes eukaryotic or prokaryotic host cells which are stably transfected with recombinant nucleic acids which can express the polypeptide or

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peptide fragment. A drug, compound, or any other agent may be screened against such transfected cells in competitive binding assays. For example, the formation of complexes between a polypeptide and the agent being tested can be measured in either viable or fixed cells.

5           The present invention thus provides methods of screening for drugs, compounds, or any other agent which can be used to treat diseases associated with UT116. These methods comprise contacting the agent with a polypeptide or fragment thereof and assaying for either the presence of a complex between the agent and the polypeptide, or for the presence of a complex between the polypeptide and the cell. In  
10 competitive binding assays, the polypeptide typically is labeled. After suitable incubation, free (or uncomplexed) polypeptide or fragment thereof is separated from that present in bound form, and the amount of free or uncomplexed label is used as a measure of the ability of the particular agent to bind to the polypeptide or to interfere with the polypeptide/cell complex.

15           The present invention also encompasses the use of competitive screening assays in which neutralizing antibodies capable of binding polypeptide specifically compete with a test agent for binding to the polypeptide or fragment thereof. In this manner, the antibodies can be used to detect the presence of any polypeptide in the test sample which shares one or more antigenic determinants with a UT116 polypeptide as  
20 provided herein.

Another technique for screening provides high throughput screening for compounds having suitable binding affinity to at least one polypeptide of UT116 disclosed herein. Briefly, large numbers of different small peptide test compounds are synthesized on a solid phase, such as plastic pins or some other surface. The peptide  
25 test compounds are reacted with polypeptide and washed. Polypeptide thus bound to the solid phase is detected by methods well-known in the art. Purified polypeptide can also be coated directly onto plates for use in the screening techniques described herein. In addition, non-neutralizing antibodies can be used to capture the polypeptide and immobilize it on the solid support. See, for example, EP 84/03564, published on  
30 September 13, 1984, which is incorporated herein by reference.

The goal of rational drug design is to produce structural analogs of biologically active polypeptides of interest or of the small molecules including agonists, antagonists, or inhibitors with which they interact. Such structural analogs can be used to design drugs which are more active or stable forms of the polypeptide or which  
35 enhance or interfere with the function of a polypeptide in vivo. J. Hodgson, Bio/Technology 9:19-21 (1991), incorporated herein by reference.

For example, in one approach, the three-dimensional structure of a polypeptide, or of a polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of a polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant structural information is used to design analogous polypeptide-like molecules or to identify efficient inhibitors

Useful examples of rational drug design may include molecules which have improved activity or stability as shown by S. Braxton et al., Biochemistry 31:7796-7801 (1992), or which act as inhibitors, agonists, or antagonists of native peptides as shown by S.B.P. Athauda et al., J Biochem. (Tokyo) 113 (6):742-746 (1993), incorporated herein by reference.

It also is possible to isolate a target-specific antibody selected by an assay as described hereinabove, and then to determine its crystal structure. In principle this approach yields a pharmacophore upon which subsequent drug design can be based. It further is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies ("anti-ids") to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-id is an analog of the original receptor. The anti-id then can be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides then can act as the pharmacophore (that is, a prototype pharmaceutical drug).

A sufficient amount of a recombinant polypeptide of the present invention may be made available to perform analytical studies such as X-ray crystallography. In addition, knowledge of the polypeptide amino acid sequence which is derivable from the nucleic acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of, or in addition to, x-ray crystallography.

Antibodies specific to a UT116 polypeptide (e.g., anti-UT116 antibodies) further may be used to inhibit the biological action of the polypeptide by binding to the polypeptide. In this manner, the antibodies may be used in therapy, for example, to treat urinary tract tissue diseases including urinary tract cancer and its metastases.

Further, such antibodies can detect the presence or absence of a UT116 polypeptide in a test sample and, therefore, are useful as diagnostic markers for the diagnosis of a urinary tract tissue disease or condition especially urinary tract cancer. Such antibodies may also function as a diagnostic marker for urinary tract tissue disease conditions, such as urinary tract cancer.

The present invention also is directed to antagonists and inhibitors of the polypeptides of the present invention. The antagonists and inhibitors are those which inhibit or eliminate the function of the polypeptide. Thus, for example, an antagonist may bind to a polypeptide of the present invention and inhibit or eliminate its function.

5 The antagonist, for example, could be an antibody against the polypeptide which eliminates the activity of a UT116 polypeptide by binding a UT116 polypeptide, or in some cases the antagonist may be an oligonucleotide. Examples of small molecule inhibitors include, but are not limited to, small peptides or peptide-like molecules.

10 The antagonists and inhibitors may be employed as a composition with a pharmaceutically acceptable carrier including, but not limited to, saline, buffered saline, dextrose, water, glycerol, ethanol and combinations thereof. Administration of UT116 polypeptide inhibitors is preferably systemic. The present invention also provides an antibody which inhibits the action of such a polypeptide.

15 Antisense technology can be used to reduce gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes for the polypeptide of the present invention, is used to design an antisense RNA oligonucleotide of from 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of  
20 the gene involved in transcription, thereby preventing transcription and the production of the UT116 polypeptide. For triple helix, see, for example, Lee et al, Nuc. Acids Res. 6:3073 (1979); Cooney et al, Science 241:456 (1988); and Dervan et al, Science 251:1360 (1991) The antisense RNA oligonucleotide hybridizes to the mRNA in vivo and blocks translation of a mRNA molecule into the UT116 polypeptide. For  
25 antisense, see, for example, Okano, J. Neurochem. 56:560 (1991); and "Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression", CRC Press, Boca Raton, Fla. (1988). Antisense oligonucleotides act with greater efficacy when modified to contain artificial internucleotide linkages which render the molecule resistant to nucleolytic cleavage. Such artificial internucleotide linkages include, but are  
30 not limited to, methylphosphonate, phosphorothiolate and phosphoroamidate internucleotide linkages.

#### Recombinant Technology.

35 The present invention provides host cells and expression vectors comprising UT116 polynucleotides of the present invention and methods for the production of the polypeptide(s) they encode. Such methods comprise culturing the host cells under conditions suitable for the expression of the UT116 polynucleotide and recovering the UT116 polypeptide from the cell culture.

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The present invention also provides vectors which include UT116 polynucleotides of the present invention, host cells which are genetically engineered with vectors of the present invention and the production of polypeptides of the present invention by recombinant techniques.

5           Host cells are genetically engineered (transfected, transduced or transformed) with the vectors of this invention which may be cloning vectors or expression vectors. The vector may be in the form of a plasmid, a viral particle, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transfected cells, or amplifying UT116  
10   gene(s). The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

          The polynucleotides of the present invention may be employed for producing a polypeptide by recombinant techniques. Thus, the polynucleotide sequence may be  
15   included in any one of a variety of expression vehicles, in particular, vectors or plasmids for expressing a polypeptide. Such vectors include chromosomal, nonchromosomal and synthetic DNA sequences, e.g., derivatives of SV40; bacterial plasmids; phage DNA; yeast plasmids; vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus and  
20   pseudorabics. However, any other plasmid or vector may be used so long as it is replicable and viable in the host.

          The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into appropriate restriction endonuclease sites by procedures known in the art. Such procedures and others are  
25   deemed to be within the scope of those skilled in the art. The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. Representative examples of such promoters include, but are not limited to, the LTR or the SV40 promoter, the E. coli lac or trp, the phage lambda P sub L promoter and other promoters known to control expression of  
30   genes in prokaryotic or eukaryotic cells or their viruses. The expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression. In addition, the expression vectors preferably contain a gene to provide a phenotypic trait for selection of transfected host cells such as dihydrofolate reductase or neomycin  
35   resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in E. coli.

The vector containing the appropriate DNA sequence as hereinabove described, as well as an appropriate promoter or control sequence, may be employed to transfect an appropriate host to permit the host to express the protein. As representative examples of appropriate hosts, there may be mentioned: bacterial cells, such as E. coli,  
5 Salmonella typhimurium; Streptomyces sp.; fungal cells, such as yeast; insect cells, such as Drosophila and Sf9; animal cells, such as CHO, COS or Bowes melanoma; plant cells, etc. The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings provided herein.

More particularly, the present invention also includes recombinant constructs  
10 comprising one or more of the sequences as broadly described above. The constructs comprise a vector, such as a plasmid or viral vector, into which a sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences including, for example, a promoter, operably linked to the sequence. Large numbers of suitable  
15 vectors and promoters are known to those of skill in the art and are commercially available. The following vectors are provided by way of example. Bacterial: pINCY (Incyte Pharmaceuticals Inc., Palo Alto, CA), pSPORT1 (Life Technologies, Gaithersburg, MD), pQE70, pQE60, pQE-9 (Qiagen) pBs, phagescript, psiX174, pBluescript SK, pBsKS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A,  
20 pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia); Eukaryotic: pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia). However, any other plasmid or vector may be used as long as it is replicable and viable in the host.

Plasmid pINCY is generally identical to the plasmid pSPORT1 (available from  
25 Life Technologies, Gaithersburg, MD) with the exception that it has two modifications in the polylinker (multiple cloning site). These modifications are (1) it lacks a HindIII restriction site and (2) its EcoRI restriction site lies at a different location. pINCY is created from pSPORT1 by cleaving pSPORT1 with both HindIII and EcoRI and replacing the excised fragment of the polylinker with synthetic DNA fragments  
30 (SEQUENCE ID NO 13 or SEQUENCE ID NO 14). This replacement may be made in any manner known to those of ordinary skill in the art. For example, the two nucleotide sequences, SEQUENCE ID NO 13 or SEQUENCE ID NO 14, may be generated synthetically with 5' terminal phosphates, mixed together, and then ligated under standard conditions for performing staggered end ligations into the pSPORT1  
35 plasmid cut with HindIII and EcoRI. Suitable host cells (such as E. coli DH5 $\mu$  cells) then are transfected with the ligated DNA and recombinant clones are selected for ampicillin resistance. Plasmid DNA then is prepared from individual clones and

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Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transfection of the host cell, e.g., the ampicillin resistance gene of E. coli and S. cerevisiae TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence.

- 5 Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), alpha factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the
- 10 periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product.

- Useful expression vectors for bacterial use are constructed by inserting a
- 15 structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transfection include E.
- 20 coli, Bacillus subtilis, Salmonella typhimurium and various species within the genera Pseudomonas, Streptomyces and Staphylococcus, although others may also be employed as a routine matter of choice.

- Useful expression vectors for bacterial use comprise a selectable marker and bacterial origin of replication derived from plasmids comprising genetic elements of the
- 25 well-known cloning vector pBR322 (ATCC 37017). Other vectors include but are not limited to PKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM1 (Promega Biotec, Madison, WI). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed.

- Following transfection of a suitable host and growth of the host to an
- 30 appropriate cell density, the selected promoter is derepressed by appropriate means (e.g., temperature shift or chemical induction), and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification. Microbial cells employed in expression of proteins can be disrupted by any convenient
- 35 method including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Such methods are well-known to the ordinary artisan.



Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts described by Gluzman, Cell 23:175 (1981), and other cell lines capable of expressing a compatible vector, such as the C127, HEK-293, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer and also any necessary ribosome binding sites, polyadenylation sites, splice donor and acceptor sites, transcriptional termination sequences and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Representative, useful vectors include pRc/CMV and pcDNA3 (available from Invitrogen, San Diego, CA).

UT116 polypeptides are recovered and purified from recombinant cell cultures by known methods including affinity chromatography, ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, hydroxyapatite chromatography or lectin chromatography. It is preferred to have low concentrations (approximately 0.1-5 mM) of calcium ion present during purification [Price, et al., J. Biol. Chem. 244:917 (1969)]. Protein refolding steps can be used, as necessary, in completing configuration of the polypeptide. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

Thus, polypeptides of the present invention may be naturally purified products expressed from a high expressing cell line, or a product of chemical synthetic procedures, or produced by recombinant techniques from a prokaryotic or eukaryotic host (for example, by bacterial, yeast, higher plant, insect and mammalian cells in culture). Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated with mammalian or other eukaryotic carbohydrates or may be non-glycosylated. The polypeptides of the invention may also include an initial methionine amino acid residue.

The starting plasmids can be constructed from available plasmids in accord with published, known procedures. In addition, equivalent plasmids to those described are known in the art and will be apparent to one of ordinary skill in the art.

The following is the general procedure for the isolation and analysis of cDNA clones. In a particular embodiment disclosed herein, mRNA was isolated from urinary tract tissue and used to generate the cDNA library. Urinary tract tissue was obtained from patients by surgical resection and was classified as tumor or non-tumor tissue by a pathologist.

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The cDNA inserts from random isolates of the urinary tract tissue libraries were sequenced in part, analyzed in detail as set forth in the Examples, and are disclosed in the Sequence Listing as SEQUENCE ID NOS 1-10. Also analyzed in detail as set forth in the Examples, and disclosed in the Sequence Listing, is the full-length  
5 sequence of clone 1543671 (referred to as clone 1543671IH (SEQUENCE ID NO 11)). The consensus sequence of these inserts is presented as SEQUENCE ID NO 12. These polynucleotides may contain an entire open reading frame with or without associated regulatory sequences for a particular gene, or they may encode only a portion of the gene of interest. This is attributed to the fact that many genes are several  
10 hundred and sometimes several thousand bases in length and, with current technology, cannot be cloned in their entirety because of vector limitations, incomplete reverse transcription of the first strand, or incomplete replication of the second strand. Contiguous, secondary clones containing additional nucleotide sequences may be obtained using a variety of methods known to those of skill in the art.

15 Methods for DNA sequencing are well known in the art. Conventional enzymatic methods employ DNA polymerase, Klenow fragment, Sequenase (US Biochemical Corp. Cleveland, OH) or Taq polymerase to extend DNA chains from an oligonucleotide primer annealed to the DNA template of interest. Methods have been developed for the use of both single-stranded and double-stranded templates. The  
20 chain termination reaction products may be electrophoresed on urea/polyacrylamide gels and detected either by autoradiography (for radionucleotide labeled precursors) or by fluorescence (for fluorescent-labeled precursors). Recent improvements in mechanized reaction preparation, sequencing and analysis using the fluorescent detection method have permitted expansion in the number of sequences that can be  
25 determined per day using machines such as the Applied Biosystems 377 DNA Sequencers (Applied Biosystems, Foster City, CA).

The reading frame of the nucleotide sequence can be ascertained by several types of analyses. First, reading frames contained within the coding sequence can be analyzed for the presence of start codon ATG and stop codons TGA, TAA or TAG.  
30 Typically, one reading frame will continue throughout the major portion of a cDNA sequence while other reading frames tend to contain numerous stop codons. In such cases, reading frame determination is straightforward. In other more difficult cases, further analysis is required.

Algorithms have been created to analyze the occurrence of individual nucleotide  
35 bases at each putative codon triplet. See, for example J.W. Fickett, Nuc. Acids Res. 10:5303 (1982). Coding DNA for particular organisms (bacteria, plants and animals) tends to contain certain nucleotides within certain triplet periodicities, such as a

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significant preference for pyrimidines in the third codon position. These preferences have been incorporated into widely available software which can be used to determine coding potential (and frame) of a given stretch of DNA. The algorithm-derived information combined with start/stop codon information can be used to determine proper frame with a high degree of certainty. This, in turn, readily permits cloning of the sequence in the correct reading frame into appropriate expression vectors.

The nucleic acid sequences disclosed herein may be joined to a variety of other polynucleotide sequences and vectors of interest by means of well-established recombinant DNA techniques. See J. Sambrook et al., supra. Vectors of interest include cloning vectors, such as plasmids, cosmids, phage derivatives, phagemids, as well as sequencing, replication and expression vectors, and the like. In general, such vectors contain an origin of replication functional in at least one organism, convenient restriction endonuclease digestion sites and selectable markers appropriate for particular host cells. The vectors can be transferred by a variety of means known to those of skill in the art into suitable host cells which then produce the desired DNA, RNA or polypeptides.

Occasionally, sequencing or random reverse transcription errors will mask the presence of the appropriate open reading frame or regulatory element. In such cases, it is possible to determine the correct reading frame by attempting to express the polypeptide and determining the amino acid sequence by standard peptide mapping and sequencing techniques. See, F.M. Ausubel et al., Current Protocols in Molecular Biology, John Wiley & Sons, New York, NY (1989). Additionally, the actual reading frame of a given nucleotide sequence may be determined by transfection of host cells with vectors containing all three potential reading frames. Only those cells with the nucleotide sequence in the correct reading frame will produce a peptide of the predicted length.

The nucleotide sequences provided herein have been prepared by current, state-of-the-art, automated methods and, as such, may contain unidentified nucleotides. These will not present a problem to those skilled in the art who wish to practice the invention. Several methods employing standard recombinant techniques, described in J. Sambrook (supra) or periodic updates thereof, may be used to complete the missing sequence information. The same techniques used for obtaining a full length sequence, as described herein, may be used to obtain nucleotide sequences.

Expression of a particular cDNA may be accomplished by subcloning the cDNA into an appropriate expression vector and transfecting this vector into an appropriate expression host. The cloning vector used for the generation of the urinary tract tissue cDNA library can be used for transcribing mRNA of a particular cDNA and

contains a promoter for beta-galactosidase, an amino-terminal met and the subsequent seven amino acid residues of beta-galactosidase. Immediately following these eight residues is an engineered bacteriophage promoter useful for artificial priming and transcription, as well as a number of unique restriction sites, including EcoRI, for cloning. The vector can be transfected into an appropriate host strain of E. coli.

Induction of the isolated bacterial strain with isopropylthiogalactoside (IPTG) using standard methods will produce a fusion protein which contains the first seven residues of beta-galactosidase, about 15 residues of linker and the peptide encoded within the cDNA. Since cDNA clone inserts are generated by an essentially random process, there is one chance in three that the included cDNA will lie in the correct frame for proper translation. If the cDNA is not in the proper reading frame, the correct frame can be obtained by deletion or insertion of an appropriate number of bases by well known methods including in vitro mutagenesis, digestion with exonuclease III or mung bean nuclease, or oligonucleotide linker inclusion.

The cDNA can be shuttled into other vectors known to be useful for expression of protein in specific hosts. Oligonucleotide primers containing cloning sites and segments of DNA sufficient to hybridize to stretches at both ends of the target cDNA can be synthesized chemically by standard methods. These primers can then be used to amplify the desired gene segments by PCR. The resulting new gene segments can be digested with appropriate restriction enzymes under standard conditions and isolated by gel electrophoresis. Alternately, similar gene segments can be produced by digestion of the cDNA with appropriate restriction enzymes and filling in the missing gene segments with chemically synthesized oligonucleotides. Segments of the coding sequence from more than one gene can be ligated together and cloned in appropriate vectors to optimize expression of recombinant sequence.

Suitable expression hosts for such chimeric molecules include, but are not limited to, mammalian cells, such as Chinese Hamster Ovary (CHO) and human embryonic kidney (HEK) 293 cells, insect cells, such as Sf9 cells, yeast cells, such as Saccharomyces cerevisiae and bacteria, such as E. coli. For each of these cell systems, a useful expression vector may also include an origin of replication to allow propagation in bacteria and a selectable marker such as the beta-lactamase antibiotic resistance gene to allow selection in bacteria. In addition, the vectors may include a second selectable marker, such as the neomycin phosphotransferase gene, to allow selection in transfected eukaryotic host cells. Vectors for use in eukaryotic expression hosts may require the addition of 3' poly A tail if the sequence of interest lacks poly A.

Additionally, the vector may contain promoters or enhancers which increase gene expression. Such promoters are host specific and include, but are not limited to,

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 217. **Figure 210**

### Immunoassays.

UT116 polypeptides, including fragments, derivatives, and analogs thereof, or cells expressing such polypeptides, can be utilized in a variety of assays, many of which are described herein, for the detection of antibodies to urinary tract tissue. They also can be used as immunogens to produce antibodies. These antibodies can be, for example, polyclonal or monoclonal antibodies, chimeric, single chain and humanized antibodies, as well as Fab fragments, or the product of an Fab expression library. Various procedures known in the art may be used for the production of such antibodies and fragments.

For example, antibodies generated against a polypeptide comprising a sequence of the present invention can be obtained by direct injection of the polypeptide into an animal or by administering the polypeptide to an animal such as a mouse, rabbit, goat or human. A mouse, rabbit or goat is preferred. The polypeptide is selected from the group consisting of SEQUENCE ID NO 25, SEQUENCE ID NO 26, SEQUENCE ID NO 27, SEQUENCE ID NO 28 and SEQUENCE ID NO 29, and fragments thereof. The antibody so obtained then will bind the polypeptide itself. In this manner, even a

sequence encoding only a fragment of the polypeptide can be used to generate antibodies that bind the native polypeptide. Such antibodies then can be used to isolate the polypeptide from test samples such as tissue suspected of containing that polypeptide. For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique as described by Kohler and Milstein, Nature 256:495-497 (1975), the trioma technique, the human B-cell hybridoma technique as described by Kozbor et al, Immun. Today 4:72 (1983) and the EBV-hybridoma technique to produce human monoclonal antibodies as described by Cole et al., in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc, New York, NY, pp. 77-96 (1985). Techniques described for the production of single chain antibodies can be adapted to produce single chain antibodies to immunogenic polypeptide products of this invention. See, for example, U.S. Patent No. 4,946,778, which is incorporated herein by reference.

Various assay formats may utilize the antibodies of the present invention, including "sandwich" immunoassays and probe assays. For example, the antibodies of the present invention, or fragments thereof, can be employed in various assay systems to determine the presence, if any, of UT116 antigen in a test sample. For example, in a first assay format, a polyclonal or monoclonal antibody or fragment thereof, or a combination of these antibodies, which has been coated on a solid phase, is contacted with a test sample, to form a first mixture. This first mixture is incubated for a time and under conditions sufficient to form antigen/antibody complexes. Then, an indicator reagent comprising a monoclonal or a polyclonal antibody or a fragment thereof, or a combination of these antibodies, to which a signal generating compound has been attached, is contacted with the antigen/antibody complexes to form a second mixture. This second mixture then is incubated for a time and under conditions sufficient to form antibody/antigen/antibody complexes. The presence of UT116 antigen in the test sample and captured on the solid phase, if any, is determined by detecting the measurable signal generated by the signal generating compound. The amount of UT116 antigen present in the test sample is proportional to the signal generated.

In an alternative assay format, a mixture is formed by contacting: (1) a polyclonal antibody, monoclonal antibody, or fragment thereof, which specifically binds to UT116 antigen, or a combination of such antibodies bound to a solid support; (2) the test sample; and (3) an indicator reagent comprising a monoclonal antibody, polyclonal antibody, or fragment thereof, which specifically binds to a different UT116 antigen (or a combination of these antibodies) to which a signal generating compound

is attached. This mixture is incubated for a time and under conditions sufficient to form antibody/antigen/antibody complexes. The presence, if any, of UT116 antigen present in the test sample and captured on the solid phase is determined by detecting the measurable signal generated by the signal generating compound. The amount of  
5 UT116 antigen present in the test sample is proportional to the signal generated.

In another assay format, one or a combination of at least two monoclonal antibodies of the invention can be employed as a competitive probe for the detection of antibodies to UT116 antigen. For example, UT116 polypeptides such as the recombinant antigens disclosed herein, either alone or in combination, are coated on a  
10 solid phase. A test sample suspected of containing antibody to UT116 antigen then is incubated with an indicator reagent comprising a signal generating compound and at least one monoclonal antibody of the invention for a time and under conditions sufficient to form antigen/antibody complexes of either the test sample and indicator reagent bound to the solid phase or the indicator reagent bound to the solid phase. The  
15 reduction in binding of the monoclonal antibody to the solid phase can be quantitatively measured.

In yet another detection method, each of the monoclonal or polyclonal antibodies of the present invention can be employed in the detection of UT116 antigens in tissue sections, as well as in cells, by immunohistochemical analysis. The tissue  
20 sections can be cut from either frozen or chemically fixed samples of tissue. If the antigens are to be detected in cells, the cells can be isolated from blood, urine, breast aspirates, or other bodily fluids. The cells may be obtained by biopsy, either surgical or by needle. The cells can be isolated by centrifugation or magnetic attraction after labeling with magnetic particles or ferrofluids so as to enrich a particular fraction of  
25 cells for staining with the antibodies of the present invention. Cytochemical analysis wherein these antibodies are labeled directly (with, for example, fluorescein, colloidal gold, horseradish peroxidase, alkaline phosphatase, etc.) or are labeled by using secondary labeled anti-species antibodies (with various labels as exemplified herein) to track the histopathology of disease also are within the scope of the present invention.

30 In addition, these monoclonal antibodies can be bound to matrices similar to CNBr-activated Sepharose and used for the affinity purification of specific UT116 polypeptides from cell cultures or biological tissues such as to purify recombinant and native UT116 proteins.

The monoclonal antibodies of the invention also can be used for the generation  
35 of chimeric antibodies for therapeutic use, or other similar applications.

The monoclonal antibodies or fragments thereof can be provided individually to detect UT116 antigens. Combinations of the monoclonal antibodies (and fragments

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thereof) provided herein also may be used together as components in a mixture or "cocktail" of at least one UT116 antibody of the invention, along with antibodies which specifically bind to other UT116 regions, each antibody having different binding specificities. Thus, this cocktail can include the monoclonal antibodies of the invention which are directed to UT116 polypeptides disclosed herein and other monoclonal antibodies specific to other antigenic determinants of UT116 antigens or other related proteins.

The polyclonal antibody or fragment thereof which can be used in the assay formats should specifically bind to a UT116 polypeptide or other UT116 polypeptides additionally used in the assay. The polyclonal antibody used preferably is of mammalian origin such as, human, goat, rabbit or sheep polyclonal antibody which binds UT116 polypeptide. Most preferably, the polyclonal antibody is of rabbit origin. The polyclonal antibodies used in the assays can be used either alone or as a cocktail of polyclonal antibodies. Since the cocktails used in the assay formats are comprised of either monoclonal antibodies or polyclonal antibodies having different binding specificity to UT116 polypeptides, they are useful for the detecting, diagnosing, staging, monitoring, prognosticating, in vivo imaging, preventing or treating, or determining the predisposition to, diseases and conditions of the urinary tract, such as urinary tract cancer.

It is contemplated and within the scope of the present invention that UT116 antigen may be detectable in assays by use of a recombinant antigen as well as by use of a synthetic peptide or purified peptide, which peptide comprises an amino acid sequence of UT116. The amino acid sequence of such a polypeptide is selected from the group consisting of SEQUENCE ID NO 25, SEQUENCE ID NO 26, SEQUENCE ID NO 27, SEQUENCE ID NO 28 and SEQUENCE ID NO 29, and fragments thereof. It also is within the scope of the present invention that different synthetic, recombinant or purified peptides, identifying different epitopes of UT116, can be used in combination in an assay for the detecting, diagnosing, staging, monitoring, prognosticating, in vivo imaging, preventing or treating, or determining the predisposition to diseases and conditions of the urinary tract, such as urinary tract cancer. In this case, all of these peptides can be coated onto one solid phase; or each separate peptide may be coated onto separate solid phases, such as microparticles, and then combined to form a mixture of peptides which can be later used in assays. Furthermore, it is contemplated that multiple peptides which define epitopes from different antigens may be used for the detection, diagnosis, staging, monitoring, prognosis, prevention or treatment of, or determining the predisposition to, diseases and conditions of the urinary tract, such as urinary tract cancer. Peptides coated on



5 The presence of UT116 antigen indicates the presence of urinary tract tissue disease, especially urinary tract cancer, in the patient. Variations of assay formats are known to those of ordinary skill in the art and many are discussed herein below.

In yet other assay formats, the polypeptides disclosed herein may be utilized to detect the presence of antibody against UT116 antigen in test samples. For example, a test sample is incubated with a solid phase to which at least one polypeptide such as a recombinant protein or synthetic peptide has been attached. The polypeptide is selected from the group consisting of SEQUENCE ID NO 25, SEQUENCE ID NO 26, SEQUENCE ID NO 27, SEQUENCE ID NO 28 and SEQUENCE ID NO 29, and fragments thereof. These are reacted for a time and under conditions sufficient to form antigen/antibody complexes. Following incubation, the antigen/antibody complex is

detected. Indicator reagents may be used to facilitate detection, depending upon the assay system chosen. In another assay format, a test sample is contacted with a solid phase to which a recombinant protein produced as described herein is attached, and also is contacted with a monoclonal or polyclonal antibody specific for the protein, which preferably has been labeled with an indicator reagent. After incubation for a time and under conditions sufficient for antibody/antigen complexes to form, the solid phase is separated from the free phase, and the label is detected in either the solid or free phase as an indication of the presence of antibody against UT116 antigen. Other assay formats utilizing the recombinant antigens disclosed herein are contemplated. These include contacting a test sample with a solid phase to which at least one antigen from a first source has been attached, incubating the solid phase and test sample for a time and under conditions sufficient to form antigen/antibody complexes, and then contacting the solid phase with a labeled antigen, which antigen is derived from a second source different from the first source. For example, a recombinant protein derived from a first source such as E. coli is used as a capture antigen on a solid phase, a test sample is added to the so-prepared solid phase, and following standard incubation and washing steps as deemed or required, a recombinant protein derived from a different source (i.e., non-E. coli) is utilized as a part of an indicator reagent which subsequently is detected. Likewise, combinations of a recombinant antigen on a solid phase and synthetic peptide in the indicator phase also are possible. Any assay format which utilizes an antigen specific for UT116 produced or derived from a first source as the capture antigen and an antigen specific for UT116 from a different second source is contemplated. Thus, various combinations of recombinant antigens, as well as the use of synthetic peptides, purified proteins and the like, are within the scope of this invention. Assays such as this and others are described in U.S. Patent No. 5,254,458, which enjoys common ownership and is incorporated herein by reference.

Other embodiments which utilize various other solid phases also are contemplated and are within the scope of this invention. For example, ion capture procedures for immobilizing an immobilizable reaction complex with a negatively charged polymer (described in EP publication 0326100 and EP publication No. 0406473), can be employed according to the present invention to effect a fast solution-phase immunochemical reaction. An immobilizable immune complex is separated from the rest of the reaction mixture by ionic interactions between the negatively charged poly-anion/immune complex and the previously treated, positively charged porous matrix and detected by using various signal generating systems previously described, including those described in chemiluminescent signal measurements as described in EPO Publication No. 0 273,115.

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Also, the methods of the present invention can be adapted for use in systems which utilize microparticle technology including automated and semi-automated systems wherein the solid phase comprises a microparticle (magnetic or non-magnetic). Such systems include those described in, for example, published EPO applications  
5 Nos. EP 0 425 633 and EP 0 424 634, respectively.

The use of scanning probe microscopy (SPM) for immunoassays also is a technology to which the monoclonal antibodies of the present invention are easily adaptable. In scanning probe microscopy, particularly in atomic force microscopy, the capture phase, for example, at least one of the monoclonal antibodies of the invention,  
10 is adhered to a solid phase and a scanning probe microscope is utilized to detect antigen/antibody complexes which may be present on the surface of the solid phase. The use of scanning tunneling microscopy eliminates the need for labels which normally must be utilized in many immunoassay systems to detect antigen/antibody complexes. The use of SPM to monitor specific binding reactions can occur in many  
15 ways. In one embodiment, one member of a specific binding partner (analyte specific substance which is the monoclonal antibody of the invention) is attached to a surface suitable for scanning. The attachment of the analyte specific substance may be by adsorption to a test piece which comprises a solid phase of a plastic or metal surface, following methods known to those of ordinary skill in the art. Or, covalent attachment  
20 of a specific binding partner (analyte specific substance) to a test piece which test piece comprises a solid phase of derivatized plastic, metal, silicon, or glass may be utilized. Covalent attachment methods are known to those skilled in the art and include a variety of means to irreversibly link specific binding partners to the test piece. If the test piece is silicon or glass, the surface must be activated prior to attaching the specific binding  
25 partner. Also, polyelectrolyte interactions may be used to immobilize a specific binding partner on a surface of a test piece by using techniques and chemistries. The preferred method of attachment is by covalent means. Following attachment of a specific binding member, the surface may be further treated with materials such as serum, proteins, or other blocking agents to minimize non-specific binding. The surface also may be  
30 scanned either at the site of manufacture or point of use to verify its suitability for assay purposes. The scanning process is not anticipated to alter the specific binding properties of the test piece.

While the present invention discloses the preference for the use of solid phases, it is contemplated that the reagents such as antibodies, proteins and peptides of the  
35 present invention can be utilized in non-solid phase assay systems. These assay systems are known to those skilled in the art, and are considered to be within the scope of the present invention.

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It is contemplated that the reagent employed for the assay can be provided in the form of a test kit with one or more containers such as vials or bottles, with each container containing a separate reagent such as a probe, primer, monoclonal antibody or a cocktail of monoclonal antibodies, or a polypeptide (e.g. recombinantly, synthetically produced or purified) employed in the assay. The polypeptide is selected from the group consisting of SEQUENCE ID NO 25, SEQUENCE ID NO 26, SEQUENCE ID NO 27, SEQUENCE ID NO 28 and SEQUENCE ID NO 29, and fragments thereof. Other components such as buffers, controls and the like, known to those of ordinary skill in art, may be included in such test kits. It also is contemplated to provide test kits which have means for collecting test samples comprising accessible body fluids, e.g., blood, urine, saliva and stool. Such tools useful for collection ("collection materials") include lancets and absorbent paper or cloth for collecting and stabilizing blood; swabs for collecting and stabilizing saliva; cups for collecting and stabilizing urine or stool samples. Collection materials, papers, cloths, swabs, cups and the like, may optionally be treated to avoid denaturation or irreversible adsorption of the sample. The collection materials also may be treated with or contain preservatives, stabilizers or antimicrobial agents to help maintain the integrity of the specimens. Test kits designed for the collection, stabilization and preservation of test specimens obtained by surgery or needle biopsy are also useful. It is contemplated that all kits may be configured in two components which can be provided separately; one component for collection and transport of the specimen and the other component for the analysis of the specimen. The collection component, for example, can be provided to the open market user while the components for analysis can be provided to others such as laboratory personnel for determination of the presence, absence or amount of analyte. Further, kits for the collection, stabilization and preservation of test specimens may be configured for use by untrained personnel and may be available in the open market for use at home with subsequent transportation to a laboratory for analysis of the test sample.

In Vivo Antibody Use.

Antibodies of the present invention can be used in vivo; that is, they can be injected into patients suspected of having diseases of the urinary tract for diagnostic or therapeutic uses. The use of antibodies for in vivo diagnosis is well known in the art. Sumerdon et al, Nucl. Med. Biol, 17, 247-254 (1990) have described an optimized antibody-chelator for the radioimmunosintographic imaging of carcinoembryonic antigen (CEA) expressing tumors using Indium-111 as the label. Griffin et al, J Clin Onc, 9, 631-640 (1991) have described the use of this agent in detecting tumors in patients suspected of having recurrent colorectal cancer. The use of similar agents with

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paramagnetic ions as labels for magnetic resonance imaging is known in the art (R. B. Lauffer, *Magnetic Resonance in Medicine*, 22, 339-342 (1991)). It is anticipated that antibodies directed against UT116 antigen can be injected into patients suspected of having a disease of the urinary tract such as urinary tract cancer for the purpose of  
5 diagnosing or staging the disease status of the patient. The label used will depend on the imaging modality chosen. Radioactive labels such as Indium-111, Technetium-99m, or Iodine-131 can be used for planar scans or single photon emission computed tomography (SPECT). Positron emitting labels such as Fluorine-19 can also be used for positron emission tomography (PET). For MRI, paramagnetic ions such as  
10 Gadolinium (III) or Manganese (II) can be used. Localization of the label within the urinary tract or external to the urinary tract may allow determination of spread of the disease. The amount of label within the urinary tract may allow determination of the presence or absence of cancer of the urinary tract.

For patients known to have a disease of the urinary tract, injection of an  
15 antibody directed against UT116 antigen may have therapeutic benefit. The antibody may exert its effect without the use of attached agents by binding to UT116 antigen expressed on or in the tissue or organ. Alternatively, the antibody may be conjugated to cytotoxic agents such as drugs, toxins, or radionuclides to enhance its therapeutic effect. Garnett and Baldwin, *Cancer Research*, 46, 2407-2412 (1986) have described  
20 the preparation of a drug-monoclonal antibody conjugate. Pastan et al, *Cell*, 47, 641-648 (1986) have reviewed the use of toxins conjugated to monoclonal antibodies for the therapy of various cancers. Goodwin and Meares, *Cancer Supplement*, 80, 2675-2680 (1997) have described the use of Yttrium-90 labeled monoclonal antibodies in various strategies to maximize the dose to tumor while limiting normal tissue toxicity.  
25 Other known cytotoxic radionuclides include Copper-67, Iodine-131, and Rhenium-186 all of which can be used to label monoclonal antibodies directed against UT116 antigen for the treatment of cancer of the bladder.

E. coli bacteria (clone 1543671) was deposited on June 25, 1997 with the American Type Culture Collection (A.T.C.C.), 12301 Parklawn Drive, Rockville,  
30 Maryland 20852. The deposit was made under the terms of the Budapest Treaty and will be maintained for a period of thirty (30) years from the date of deposit, or for five (5) years after the last request for the deposit, or for the enforceable period of the U.S. patent, whichever is longer. This deposit, and any other deposited material described herein, are provided for convenience only, and are not required to practice  
35 the present invention in view of the teachings provided herein. The cDNA sequence in all of the deposited material is incorporated herein by reference. Clone 1543671 was accorded A.T.C.C. Deposit No. 98465.

The present invention will now be described by way of examples, which are meant to illustrate, but not to limit, the scope of the present invention.

### EXAMPLES

5     Example 1: Identification of Urinary Tract Tissue Library UT116 Gene-Specific  
          Clones

A. Library Comparison of Expressed Sequence Tags (EST's) or Transcript  
          Images. Partial sequences of cDNA clone inserts, so-called "expressed sequence tags"  
          (EST's), were derived from cDNA libraries made from urinary tract tumor tissues,  
10     urinary tract -non-tumor tissues and numerous other tissues, both tumor and non-tumor  
          and entered into a database (LIFESEQ™ database, available from Incyte  
          Pharmaceuticals, Palo Alto, CA) as gene transcript images. See International  
          Publication No. WO 95/20681. (A transcript image is a listing of the number of EST's  
15     for each of the represented genes in a given tissue library. EST's sharing regions of  
          mutual sequence overlap are classified into clusters. A cluster is assigned a clone  
          number from a representative 5' EST. Often, a cluster of interest can be extended by  
          comparing its consensus sequence with sequences of other EST's which did not meet  
          the criteria for automated clustering. The alignment of all available clusters and single  
20     EST's represent a contig from which a consensus sequence is derived.) The transcript  
          images then were evaluated to identify EST sequences that were representative  
          primarily of the urinary tract tissue libraries. These target clones then were ranked  
          according to their abundance (occurrence) in the target libraries and their absence from  
          background libraries. Higher abundance clones with low background occurrence were  
          given higher study priority. EST's corresponding to the consensus sequence of  
25     UT116 were found in 78.5% (11 of 14) of urinary tract tissue libraries. EST's  
          corresponding to the consensus sequence SEQUENCE ID NO 12 (or fragments  
          thereof) were found in only 4.2% (27 of 638) of the other, non-urinary tract, libraries  
          of the data base. Therefore, the consensus sequence or fragment thereof was found  
          more than 18 times more often in urinary tract than non-urinary tract tissues.  
30     Overlapping clones 3353644 (SEQUENCE ID NO 1), 2804743 (SEQUENCE ID NO  
          2), 1891065 (SEQUENCE ID NO 3), 1543671 (SEQUENCE ID NO 4), 1863905  
          (SEQUENCE ID NO 5), 1314679 (SEQUENCE ID NO 6), 1901337 (SEQUENCE ID  
          NO 7), 1900086 (SEQUENCE ID NO 8), 2325070 (SEQUENCE ID NO 9), and  
          3969672 (SEQUENCE ID NO 10), respectively, were identified for further study.  
35     These represented the minimum number of clones that were needed to form the contig  
          and from which, along with the full-length sequence of clone 1543671IH

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(SEQUENCE ID NO 11), the consensus sequence provided herein (SEQUENCE ID NO 12) was derived.

5        B. Generation of a Consensus Sequence. The nucleotide sequences of clones 3353644 (SEQUENCE ID NO 1), 2804743 (SEQUENCE ID NO 2), 1891065 (SEQUENCE ID NO 3), 1543671 (SEQUENCE ID NO 4), 1863905 (SEQUENCE ID NO 5), 1314679 (SEQUENCE ID NO 6), 1901337 (SEQUENCE ID NO 7), 1900086 (SEQUENCE ID NO 8), 2325070 (SEQUENCE ID NO 9), 3969672 (SEQUENCE ID NO 10), and 1543671IH (SEQUENCE ID NO 11) were entered in the Sequencher™ Program (available from Gene Codes Corporation, Ann Arbor, MI), in order to  
10        generate a nucleotide alignment (contig map) and then generate their consensus sequence (SEQUENCE ID NO 12). Figures 1A-1C show the nucleotide sequence alignment of these clones and their resultant nucleotide consensus sequence (SEQUENCE ID NO 12). Figure 2 presents the contig map depicting the clones 3353644 (SEQUENCE ID NO 1), 2804743 (SEQUENCE ID NO 2), 1891065  
15        (SEQUENCE ID NO 3), 1543671 (SEQUENCE ID NO 4), 1863905 (SEQUENCE ID NO 5), 1314679 (SEQUENCE ID NO 6), 1901337 (SEQUENCE ID NO 7), 1900086 (SEQUENCE ID NO 8), 2325070 (SEQUENCE ID NO 9), 3969672 (SEQUENCE ID NO 10) and 1543671IH (SEQUENCE ID NO 11) which form overlapping regions of the UT116 gene, and the resultant consensus nucleotide sequence (SEQUENCE ID NO  
20        12) of these clones in a graphic display. Following this, a three-frame translation was performed on the consensus sequence (SEQUENCE ID NO 12). The first forward frame was found to have an open reading frame encoding a 123 residue amino acid sequence which is presented as SEQUENCE ID NO 25. The 123 residue amino acid sequence depicted in SEQUENCE ID NO 12 was compared with published sequences  
25        using software and techniques known to those skilled in the art. The polypeptide sequence of a 126-amino acid chicken stem cell antigen termed SCA2 was found to have some homology with the UT116 polypeptide of SEQUENCE ID NO 12. The SCA2 antigen also bears some homology with an antigen expressed by mammalian thymic blast cells. The sequence for the chicken SCA2 antigen is deposited with  
30        GenBank under Accession No. L34554.

      Analysis of the LIFESEQ™ database indicates a possible T/C polymorphism at position 59 in the consensus nucleotide sequence (SEQUENCE ID NO 12). There were 38 occurrences of the T nucleotide variant and four occurrences of the C nucleotide variant in the database. This polymorphism at nucleotide 59 results in an  
35        amino acid shift between methionine (ATG) and threonine (ACC). Because the methionine codon would be essential for initiation of protein synthesis, mRNAs comprising a C-containing variant should fail to result in protein.

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Example 2: Sequencing of UT116 EST-Specific Clones

The full-length DNA sequence of clone 1543671IH (SEQUENCE ID NO 11) of the UT116 gene contig was determined using dideoxy termination sequencing with dye terminators following known methods (F. Sanger et al., PNAS U.S.A. 74:5463 (1977)).

Because the pINCY vector (available from Incyte Pharmaceuticals, Inc., Palo Alto, CA) contains universal priming sites just adjacent to the 3' and 5' ligation junctions of the inserts, approximately 300 bases of the insert were sequenced in both directions using two universal primers (SEQUENCE ID NO 15 and SEQUENCE ID NO 16, available from New England Biolabs, Beverly, MA, and Applied Biosystems Inc, Foster City, CA, respectively). The sequencing reactions were run on a polyacrylamide denaturing gel, and the sequences were determined by an Applied Biosystems 377 Sequencer (available from Applied Biosystems, Foster City, CA). Additional sequencing primers (SEQUENCE ID NOS 17-22) were designed from sequence information of the consensus sequence (SEQUENCE ID NO 12). These primers then were used to determine the remaining DNA sequence of the cloned insert from each DNA strand, as previously described.

Example 3: Nucleic Acid

A. RNA Extraction from Tissue. Total RNA was isolated from urinary tract tissues and from non-urinary tract tissues. Various methods were utilized, including, but not limited to, the lithium chloride/urea technique, known in the art and described by Kato et al. (J. Virol. 61:2182-2191, 1987), and TRIzol™ (Gibco-BRL, Grand Island, NY).

Briefly, tissue was placed in a sterile conical tube on ice and 10-15 volumes of 3 M LiCl, 6 M urea, 5 mM EDTA, 0.1 M  $\beta$ -mercaptoethanol, 50 mM Tris-HCl (pH 7.5) were added. The tissue was homogenized with a Polytron® homogenizer (Brinkman Instruments, Inc., Westbury, NY) for 30-50 sec on ice. The solution was transferred to a 15 ml plastic centrifuge tube and placed overnight at -20°C. The tube was centrifuged for 90 min at 9,000 x g at 0-4°C and the supernatant was immediately decanted. Ten ml of 3 M LiCl were added and the tube was vortexed for 5 sec. The tube was centrifuged for 45 min at 11,000 x g at 0-4°C. The decanting, resuspension in LiCl, and centrifugation was repeated and the final pellet was air dried and suspended in 2 ml of 1 mM EDTA, 0.5% SDS, 10 mM Tris (pH 7.5). Twenty microliters (20  $\mu$ l) of Proteinase K (20 mg/ml) were added, and the solution was incubated for 30 min at 37°C with occasional mixing. One-tenth volume (0.22-0.25



ml) of 3 M NaCl was added and the solution was vortexed before transfer into another tube containing 2 ml of phenol/chloroform/isoamyl alcohol (PCI). The tube was vortexed for 1-3 sec and centrifuged for 20 min at 3,000 x g at 10°C. The PCI extraction was repeated and followed by two similar extractions with

5 chloroform/isoamyl alcohol (CI). The final aqueous solution was transferred to a prechilled 15 ml Corex glass tube containing 6 ml of absolute ethanol, the tube was covered with parafilm, and placed at -20°C overnight. The tube was centrifuged for 30 min at 10,000 x g at 0-4°C and the ethanol supernatant was decanted immediately. The RNA pellet was washed four times with 10 ml of 75% ice-cold ethanol and the final

10 pellet was air dried for 15 min at room temperature. The RNA was suspended in 0.5 ml of 10 mM TE (pH 7.6, 1 mM EDTA) and its concentration was determined spectrophotometrically. RNA samples were aliquoted and stored at -70°C as ethanol precipitates.

The quality of the RNA was determined by agarose gel electrophoresis (see Example 5, Northern Blot Analysis) and staining with 0.5 µg/ml ethidium bromide for one hour. RNA samples that did not contain intact rRNAs were excluded from the study.

Alternatively, for RT-PCR analysis, 1 ml of Ultraspec RNA reagent was added to 120 mg of pulverized tissue in a 2.0 ml polypropylene microfuge tube, homogenized with a Polytron® homogenizer (Brinkman Instruments, Inc., Westbury, NY) for 50 sec and placed on ice for 5 min. Then, 0.2 ml of chloroform was added to each sample, followed by vortexing for 15 sec. The sample was placed on ice for another 5 min, followed by centrifugation at 12,000 x g for 15 min at 4°C. The upper layer was collected and transferred to another RNase-free 2.0 ml microfuge tube. An equal volume of isopropanol was added to each sample, and the solution was placed on ice for 10 min. The sample was centrifuged at 12,000 x g for 10 min at 4°C, and the supernatant was discarded. The remaining pellet was washed twice with cold 75% ethanol, resuspended by vortexing, and the resuspended material was then pelleted by centrifugation at 7500 x g for 5 min at 4°C. Finally, the RNA pellet was dried in a Speedvac (Savant, Farmingdale, NY) for 5 min and reconstituted in RNase-free water.

**B. RNA Extraction from Blood Mononuclear Cells.** Mononuclear cells are isolated from blood samples from patients by centrifugation using Ficoll-Hypaque as follows. A 10 ml volume of whole blood is mixed with an equal volume of RPMI Medium (Gibco-BRL, Grand Island, NY). This mixture is then underlayered with 10 ml of Ficoll-Hypaque (Pharmacia, Piscataway, NJ) and centrifuged for 30 minutes at 200 x g. The buffy coat containing the mononuclear cells is removed, diluted to 50 ml with Dulbecco's PBS (Gibco-BRL, Grand Island, NY) and the mixture centrifuged for 10

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minutes at 200 x g. After two washes, the resulting pellet is resuspended in Dulbecco's PBS to a final volume of 1 ml.

RNA is prepared from the isolated mononuclear cells as described by N. Kato et al., J. Virology 61: 2182-2191 (1987). Briefly, the pelleted mononuclear cells are brought to a final volume of 1 ml and then are resuspended in 250  $\mu$ L of PBS and mixed with 2.5 ml of 3 M LiCl, 6 M urea, 5 mM EDTA, 0.1 M 2-mercaptoethanol, 50 mM Tris-HCl (pH 7.5). The resulting mixture is homogenized and incubated at -20°C overnight. The homogenate is centrifuged at 8,000 RPM in a Beckman J2-21M rotor for 90 minutes at 0-4°C. The pellet is resuspended in 10 ml of 3 M LiCl by vortexing and then centrifuged at 10,000 RPM in a Beckman J2-21M rotor centrifuge for 45 minutes at 0-4°C. The resuspending and pelleting steps then are repeated. The pellet is resuspended in 2 ml of 1 mM EDTA, 0.5% SDS, 10 mM Tris (pH 7.5) and 400  $\mu$ g Proteinase K with vortexing and then it is incubated at 37°C for 30 minutes with shaking. One tenth volume of 3 M NaCl then is added and the mixture is vortexed. Proteins are removed by two cycles of extraction with phenol/ chloroform/ isoamyl alcohol (PCI) followed by one extraction with chloroform/ isoamyl alcohol (CI). RNA is precipitated by the addition of 6 ml of absolute ethanol followed by overnight incubation at -20°C. After the precipitated RNA is collected by centrifugation, the pellet is washed 4 times in 75% ethanol. The pelleted RNA is then dissolved in solution containing 1 mM EDTA, 10 mM Tris-HCl (pH 7.5).

Non-urinary tract tissues are used as negative controls. The mRNA can be further purified from total RNA by using commercially available kits such as oligo dT cellulose spin columns (RediCol™ from Pharmacia, Uppsala, Sweden) for the isolation of poly-adenylated RNA. Total RNA or mRNA can be dissolved in lysis buffer (5 M guanidine thiocyanate, 0.1 M EDTA, pH 7.0) for analysis in the ribonuclease protection assay.

C. RNA Extraction from polysomes. Tissue is minced in saline at 4°C and mixed with 2.5 volumes of 0.8 M sucrose in a TK<sub>150</sub>M (150 mM KCl, 5 mM MgCl<sub>2</sub>, 50 mM Tris-HCl, pH 7.4) solution containing 6 mM 2-mercaptoethanol. The tissue is homogenized in a Teflon-glass Potter homogenizer with five strokes at 100-200 rpm followed by six strokes in a Dounce homogenizer, as described by B. Mechler, Methods in Enzymology 152:241-248 (1987). The homogenate then is centrifuged at 12,000 x g for 15 min at 4°C to sediment the nuclei. The polysomes are isolated by mixing 2 ml of the supernatant with 6 ml of 2.5 M sucrose in TK<sub>150</sub>M and layering this mixture over 4 ml of 2.5 M sucrose in TK<sub>150</sub>M in a 38 ml polyallomer tube. Two additional sucrose TK<sub>150</sub>M solutions are successively layered onto the extract fraction; a first layer of 13 ml 2.05 M sucrose followed by a second layer of 6 ml of 1.3 M

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sucrose. The polysomes are isolated by centrifuging the gradient at 90,000 x g for 5 hr at 4°C. The fraction then is taken from the 1.3 M sucrose/2.05 M sucrose interface with a siliconized pasteur pipette and diluted in an equal volume of TE (10 mM Tris-HCl, pH 7.4, 1 mM EDTA). An equal volume of 90°C SDS buffer (1% SDS, 200 mM NaCl, 20 mM Tris-HCl, pH 7.4) is added and the solution is incubated in a boiling water bath for 2 min. Proteins next are digested with a Proteinase-K digestion (50 mg/ml) for 15 min at 37°C. The mRNA is purified with 3 equal volumes of phenol-chloroform extractions followed by precipitation with 0.1 volume of 2 M sodium acetate (pH 5.2) and 2 volumes of 100% ethanol at -20°C overnight. The precipitated RNA is recovered by centrifugation at 12,000 x g for 10 min at 4°C. The RNA is dried and resuspended in TE (pH 7.4) or distilled water. The resuspended RNA then can be used in a slot blot or dot blot hybridization assay to check for the presence of UT116 mRNA (see Example 6, Dot Blot/Slot Blot).

The quality of nucleic acid and proteins is dependent on the method of preparation used. Each sample may require a different preparation technique to maximize isolation efficiency of the target molecule. These preparation techniques are within the skill of the ordinary artisan.

#### Example 4: Ribonuclease Protection Assay

20     A. Synthesis of Labeled Complementary RNA (cRNA) Hybridization Probe and Unlabeled Sense Strand. Labeled antisense and unlabeled sense riboprobes were transcribed from the UT116 gene cDNA sequence flanked by opposed SP6 and T7 RNA polymerase promoters. The sequence was from a vector (pSPORT 1, Life Technologies, Inc. Gaithersburg, MD) containing the appropriate UT116 cDNA insert.

25     The described plasmid, clone 1543671, which contains the UT116 gene cDNA sequence flanked by opposed SP6 and T7 RNA polymerase promoters, was purified using a Qiagen Plasmid Purification Kit (Qiagen, Chatsworth, CA). Then, 10 µg of the plasmid DNA was linearized by cutting with restriction enzyme SalI for 1 hr at 37°C. The linearized plasmid DNA was purified using the QIAquick kit (Qiagen, Chatsworth, CA) and 250 ng was used for the synthesis of antisense transcript from the SP6 promoter using the Riboprobe® in vitro Transcription System (Promega Corporation, Madison, WI) as described by the supplier's instructions, incorporating 9.3 µM (alpha-<sup>32</sup>P) CTP (Amersham Life Sciences, Inc. Arlington Heights, IL) as a label. To generate the sense strand, 10 µg of the purified plasmid DNA was cut with restriction enzymes XbaI and NotI, and 250 ng was transcribed as above from the T7 promoter except with 500 µM unlabeled CTP. Both sense and antisense strands were purified by spin column chromatography. Unlabeled sense strand was quantitated by

UV absorption at 260 nm.

5        B. Hybridization of Labeled Probe to Target. Frozen tissue was pulverized to powder under liquid nitrogen and 100-500 mg was dissolved in an appropriate volume of lysis buffer, available as a component of the Qiagen RNeasy Total RNA kit (Qiagen, Chatsworth, CA). Further dissolution was achieved using a tissue homogenizer. RNA was then isolated as described by the supplier's instructions. In addition, a dilution series of a known amount of sense strand in yeast RNA (Qiagen, Chatsworth, CA) was made for use as a positive control. Finally, 5 µg of tissue RNA or diluted sense strand was mixed directly with  $1 \times 10^5$  cpm of radioactively labeled probe, precipitated with ammonium acetate and ethanol, and suspended in 20 µl hybridization buffer, a component of the RPA II<sup>TM</sup> Ribonuclease Protection Assay kit (Ambion, Inc., Austin, TX). Hybridization was allowed to proceed overnight at 45°C. See, J.J. Lee et al., Meth. Enzymol. 152:633-648 (1987).

10        C. RNase Digestion. RNA that was not hybridized to probe was removed from the reaction as per the RPA II<sup>TM</sup> protocol using a solution of RNase A and RNase T1 for 30 min at 37°C. Hybridized fragments protected from digestion were then precipitated as described by the supplier's instructions. The precipitates were collected by centrifugation at 12,000 x g for 20 min.

15        D. Fragment Analysis. The precipitates were dissolved in denaturing gel loading dye (80% formamide, 10 mM EDTA (pH 8.0), 1 mg/ml xylene cyanol, 1 mg/ml bromophenol blue), heat denatured, and electrophoresed in 6% polyacrylamide TBE, 8 M urea denaturing gels. The gels were imaged and analyzed using the STORM<sup>TM</sup> storage phosphor autoradiography system (Molecular Dynamics, Sunnyvale, CA). Quantitation of protected fragment bands was achieved by comparing the peak areas obtained from the test samples to those from the known dilutions of the positive control sense strand (see Section B, supra). The results were expressed in pg of UT116 RNA/µg total RNA and as an image rating score (Table 1).

20        Detection of a product comprising a sequence selected from the group consisting of SEQUENCE ID NOS 1-12, and fragments or complements thereof, is indicative of the presence of UT116 mRNAs, suggesting a diagnosis of a urinary tract tissue disease or condition, such as urinary tract cancer.

25       

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Table 1. Ribonuclease Protection Results

<u>TISSUE</u>	<u>UT116 RNA (pg)/RNA(μg)</u>	<u>SCORE</u>
Normal Bladder	0	-
Normal Bladder	0	-
Normal Bladder	0	-
Bladder Cancer	0	-
Bladder Cancer	22	3+
Bladder Cancer	0	-
Bladder Cancer	0	-
Normal Prostate	0	-
Normal Prostate	0	-
Normal Prostate	8	+
Normal Prostate	0	-
Prostate Cancer	0	-
Prostate Cancer	0	-
Prostate Cancer	0	-
Prostate Cancer	0	-
Normal Colon	0	-
Normal Lung	0	-
Breast Cancer	0	-
Peripheral blood mononuclear cells	0	-
LNCaP cells	0	-
T47D cells	0	-

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Example 5: Northern Blotting

The Northern blot technique is used to identify a specific size RNA species in a complex population of RNA using agarose gel electrophoresis and nucleic acid hybridization. Briefly, 5-10 μg of total RNA (see Example 3, Nucleic Acid Preparation) were incubated in 15 μl of a solution containing 40 mM morpholinopropanesulfonic acid (MOPS) (pH 7.0), 10 mM sodium acetate, 1 mM EDTA, 2.2 M formaldehyde, 50% v/v formamide for 15 min at 65°C. The denatured RNA was mixed with 2 μl of loading buffer (50% glycerol, 1 mM EDTA, 0.4% bromophenol blue, 0.4% xylene cyanol) and loaded into a denaturing 1.0% agarose gel

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containing 40 mM MOPS (pH 7.0), 10 mM sodium acetate, 1 mM EDTA and 2.2 M formaldehyde. The gel was electrophoresed at 60 V for 1.5 hr, stained with 0.5 µg/ml ethidium bromide for one hour and rinsed in RNase free water for 30-45 min. RNA was transferred from the gel onto nylon membranes (Brightstar-Plus, Ambion, Inc., Austin, TX) for 1.5 hours using the downward alkaline capillary transfer method (Chomczynski. Anal. Biochem. 201:134-139, 1992). The filter was rinsed with 1X SSC and RNA was crosslinked to the filter using a Stratalinker (Stratagene, Inc., La Jolla, CA) on the autocrosslinking mode and dried for 15 min. The membrane was then placed into a hybridization tube containing 20 ml of preheated prehybridization solution (5X SSC, 50% formamide, 5X Denhardt's solution, 100 µg/ml denatured salmon sperm DNA) and incubated in a 42°C hybridization oven for at least 3 hr. While the blot was prehybridizing, a <sup>32</sup>P-labeled random-primed probe was generated using the UT116 insert, according to the manufacturer's instructions (Gibco-BRL, Grand Island, NY). Half of the probe was boiled for 10 min, quick chilled on ice and added to the hybridization tube. Hybridization was carried out at 42°C for at least 12 hr. The hybridization solution was discarded and the filter was washed twice in 30 ml of 3X SSC, 0.1% SDS at 42°C for 15 min, followed by two washes in 30 ml of 0.3X SSC, 0.1% SDS at 60°C for 15 min. each. The filter was wrapped in Saran Wrap and exposed to Kodak XAR-Omat film for 8-120 hr and the film was developed for analysis.

Results of the analysis of UT116 hybridization to a Northern blot containing normal bladder tissues and bladder cancer tissues are shown in Figure 3 which contains an ethidium bromide (EtBr)-stained RNA gel and the UT116 Northern blot. The positions of RNA size standards (in kb) are shown to the left of each panel. As shown, the UT116 probe detected an approximately 1.0 kb RNA in four normal bladder samples (lanes 1 - 4) and two bladder cancer tissues (lanes 8 and 9). Lane 12, containing the positive control of RNA isolated from E. coli containing a UT116 plasmid, was also positive for the UT116 hybridization.

Detection of a product comprising a sequence selected from the group consisting of SEQUENCE ID NOS 1-12, and fragments or complements thereof, is indicative of the presence of UT116 mRNAs, suggesting a diagnosis of a urinary tract tissue disease or condition, such as urinary tract cancer.

#### Example 6: Dot Blot/Slot Blot

Dot and slot blot assays are quick methods to evaluate the presence of a specific nucleic acid sequence in a complex mix of nucleic acid. To perform such assays, up to 50 µg of RNA are mixed in 50 µl of 50% formamide, 7% formaldehyde, 1X SSC,

incubated 15 min at 68°C, and then cooled on ice. Then, 100 µl of 20X SSC are added to the RNA mixture and loaded under vacuum onto a manifold apparatus that has a prepared nitrocellulose or nylon membrane. The membrane is soaked in water, 20X SSC for 1 hour, placed on two sheets of 20X SSC prewet Whatman #3 filter paper, and loaded into a slot blot or dot blot vacuum manifold apparatus. The slot blot is analyzed with probes prepared and labeled as described in Example 4, supra. Detection of mRNA corresponding to a sequence selected from the group consisting of SEQUENCE ID NOS 1-12, and fragments or complements thereof, is an indication of the presence of UT116, suggesting a diagnosis of a urinary tract tissue disease or condition, such as urinary tract cancer.

Other methods and buffers which can be utilized in the methods described in Examples 5 and 6, but not specifically detailed herein, are known in the art and are described in J. Sambrook et al, supra which is incorporated herein by reference.

#### Example 7: In Situ Hybridization

This method is useful to directly detect specific target nucleic acid sequences in cells using detectable nucleic acid hybridization probes.

Tissues are prepared with cross-linking fixative agents such as paraformaldehyde or glutaraldehyde for maximum cellular RNA retention. See, L. Angerer et al., Methods in Cell Biol. 35:37-71 (1991). Briefly, the tissue is placed in greater than 5 volumes of 1% glutaraldehyde in 50 mM sodium phosphate, pH 7.5 at 4°C for 30 min. The solution is changed with fresh glutaraldehyde solution (1% glutaraldehyde in 50mM sodium phosphate, pH 7.5) for a further 30 min fixing. The fixing solution should have an osmolality of approximately 0.375% NaCl. The tissue is washed once in isotonic NaCl to remove the phosphate.

The fixed tissues then are embedded in paraffin as follows. The tissue is dehydrated through a series of increasing ethanol concentrations for 15 min each: 50% (twice), 70% (twice), 85%, 90% and then 100% (twice). Next, the tissue is soaked in two changes of xylene for 20 min each at room temperature. The tissue is then soaked in two changes of a 1:1 mixture of xylene and paraffin for 20 min each at 60°C; and then in three final changes of paraffin for 15 min each.

Next, the tissue is cut in 5 µm sections using a standard microtome and placed on a slide previously treated with a tissue adhesive such as 3-aminopropyltriethoxysilane.

Paraffin is removed from the tissue by two 10 min xylene soaks and rehydrated in a series of decreasing ethanol concentrations: 99% (twice), 95%, 85%, 70%, 50%,

and 30%, and then in distilled water (twice). The sections are pre-treated with 0.2 M HCl for 10 min and permeabilized with 2 µg/ml Proteinase-K at 37°C for 15 min.

Labeled riboprobes transcribed from the UT116 gene plasmid (see Example 4) are hybridized to the prepared tissue sections and incubated overnight at 56°C in 3X standard saline extract and 50% formamide. Excess probe is removed by washing in 2X standard saline citrate and 50% formamide followed by digestion with 100 µg/ml RNase A at 37°C for 30 min. Fluorescence probe is visualized by illumination with ultraviolet (UV) light under a microscope. Fluorescence in the cytoplasm is indicative of UT116 mRNA. Alternatively, the sections can be visualized by autoradiography.

#### Example 8: Reverse Transcription PCR

A. One Step RT-PCR Assay. Target-specific primers are designed to detect the above-described target sequences by reverse transcription PCR using methods known in the art. One step RT-PCR is a sequential procedure that performs both RT and PCR in a single reaction mixture. The procedure is performed in a 200 µl reaction mixture containing 50 mM (N,N,-bis[2-Hydroxyethyl]glycine), pH 8.15, 81.7 mM KOAc, 33.33 mM KOH, 0.01 mg/ml bovine serum albumin, 0.1 mM ethylene diaminetetraacetic acid, 0.02 mg/ml NaN<sub>3</sub>, 8% w/v glycerol, 150 µM each of dNTP, 0.25 µM each primer, 5U rTth polymerase, 3.25 mM Mn(OAc)<sub>2</sub> and 5 µl of target RNA (see Example 3). Since RNA and the rTth polymerase enzyme are unstable in the presence of Mn(OAc)<sub>2</sub>, the Mn(OAc)<sub>2</sub> should be added just before target addition. Optimal conditions for cDNA synthesis and thermal cycling readily can be determined by those skilled in the art. The reaction is incubated in a Perkin-Elmer Thermal Cycler 480. Optimal conditions for cDNA synthesis and thermal cycling can readily be determined by those skilled in the art. Conditions which may be found useful include cDNA synthesis at 60°-70°C for 15-45 min and 30-45 amplification cycles at 94°C, 1 min; 55°-70°C, 1 min; 72°C, 2 min. One step RT-PCR also may be performed by using a dual enzyme procedure with Taq polymerase and a reverse transcriptase enzyme, such as MMLV or AMV RT enzymes.

B. Traditional RT-PCR. A traditional two-step RT-PCR reaction was performed, as described by K.Q. Hu et al., Virology 181:721-726 (1991). Briefly 1.0 µg of extracted mRNA (see Example 3) was reverse transcribed in a 20 µl reaction mixture containing 1X PCR II buffer (Perkin-Elmer Corp. part of Roche Molecular Systems, Inc., Branchburg, NJ.), 5 mM MgCl<sub>2</sub>, 1 mM dNTP, 20 U RNasin, 2.5 µM random hexamers, and 50 U MMLV (Moloney murine leukemia virus) reverse transcriptase (RT). Reverse transcription was performed at room temperature for 10 min, 42°C for 30 min in a PE-480 thermal cycler, followed by further incubation at



95°C for 5 min to inactivate the RT. PCR was performed using 2 µl of the cDNA reaction in a final PCR reaction volume of 50 µl containing 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 1.5 mM MgCl<sub>2</sub>, 200 µM dNTP, 0.4 µM of each sense and antisense primer, (SEQUENCE ID NO 23 and SEQUENCE ID NO 24, respectively), and 2.5 U of Taq polymerase. The reaction was incubated in an MJ Research Model PTC-200 as follows: Denaturation at 94 °C for 2 min. followed by 35 cycles of amplification (94°C, 45 sec; 62 °C, 45 sec; 72°C, 2 min ); a final extension (72°C, 5 min); and a soak at 4°C.

C. PCR Fragment Analysis. The correct products were verified by size determination using gel electrophoresis with a SYBR® Green I nucleic acid gel stain (Molecular Probes, Eugene, OR). Gels were stained with SYBR® Green I at a 1:10,000 dilution in 1X TBE for 30 minutes. Gels were imaged using a STORM imaging system. A number of tissue samples were analyzed, more particularly, 3 prostate cancer tissue samples, 2 prostate BPH tissue samples, 3 bladder cancer tissue samples, 2 bladder normal tissue samples, 3 colon tissue samples, 3 breast tissue samples, and 3 lung tissue samples. There was weak evidence for UT116-specific PCR amplification product in 2 of the bladder cancer tissue samples and in 1 of the prostate cancer tissue samples.

Detection of a product comprising a sequence selected from the group consisting of SEQUENCE ID NOS 1-12 and fragments or complements thereof, is indicative of the presence of UT116 mRNAs, suggesting a diagnosis of a urinary tract tissue disease or condition, such as urinary tract cancer.

#### Example 9: OH-PCR

A. Probe selection and Labeling. Target-specific primers and probes are designed to detect the above-described target sequences by oligonucleotide hybridization PCR. International Publication Nos WO 92/10505, published 25 June 1992, and WO 92/11388, published 9 July 1992, teach methods for labeling oligonucleotides at their 5' and 3' ends, respectively. According to one known method for labeling an oligonucleotide, a label-phosphoramidite reagent is prepared and used to add the label to the oligonucleotide during its synthesis. For example, see N. T. Thuong et al., Tet. Letters 29(46):5905-5908 (1988); or J. S. Cohen et al., published U.S. Patent Application 07/246,688 (NTIS ORDER No. PAT-APPL-7-246,688) (1989). Preferably, probes are labeled at their 3' end to prevent participation in PCR and the formation of undesired extension products. For one step OH-PCR, the probe should have a T<sub>M</sub> at least 15°C below the T<sub>M</sub> of the primers. The primers and probes are utilized as specific binding members, with or without detectable labels, using

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standard phosphoramidite chemistry and/or post-synthetic labeling methods which are well-known to one skilled in the art.

5        B. One Step Oligo Hybridization PCR. OH-PCR is performed on a 200 µl reaction containing 50 mM (N,N-bis[2-Hydroxyethyl]glycine), pH 8.15, 81.7 mM KOAc, 33.33 mM KOH, 0.01 mg/ml bovine serum albumin, 0.1 mM ethylene diaminetetraacetic acid, 0.02 mg/ml NaN<sub>3</sub>, 8% w/v glycerol, 150 µM each of dNTP, 0.25 µM each primer, 3.75 nM probe, 5U rTth polymerase, 3.25 mM Mn(OAc)<sub>2</sub> and 5 µl blood equivalents of target (see Example 3). Since RNA and the rTth polymerase enzyme are unstable in the presence of Mn(OAc)<sub>2</sub>, the Mn(OAc)<sub>2</sub> should be added just before target addition. The reaction is incubated in a Perkin-Elmer Thermal Cycler 480. Optimal conditions for cDNA synthesis and thermal cycling can be readily determined by those skilled in the art. Conditions which may be found useful include cDNA synthesis (60°C, 30 min), 30-45 amplification cycles (94°C, 40 sec; 55-70°C, 60 sec), oligo-hybridization (97°C, 5 min; 15°C, 5 min; 15°C soak). The correct reaction product contains at least one of the strands of the PCR product and an internally hybridized probe.

15        C. OH-PCR Product Analysis. Amplified reaction products are detected on an LCx<sup>®</sup> analyzer system (available from Abbott Laboratories, Abbott Park, IL). Briefly, the correct reaction product is captured by an antibody labeled microparticle at a 20        capturable site on either the PCR product strand or the hybridization probe, and the complex is detected by binding of a detectable antibody conjugate to either a detectable site on the probe or the PCR strand. Only a complex containing a PCR strand hybridized with the internal probe is detectable. The detection of this complex then is indicative of the presence of UT116 mRNA, suggesting a diagnosis of a urinary tract 25        disease or condition, such as urinary tract cancer.

Many other detection formats exist which can be used and/or modified by those skilled in the art to detect the presence of amplified or non-amplified UT116-derived nucleic acid sequences including, but not limited to, ligase chain reaction (LCR, Abbott Laboratories, Abbott Park, IL): Q-beta replicase (Gene-Trak<sup>™</sup>, Naperville, Illinois), 30        branched chain reaction (Chiron, Emeryville, CA) and strand displacement assays (Becton Dickinson, Research Triangle Park, NC).

#### Example 10: Synthetic Peptide Production

35        Synthetic peptides were modeled and then prepared based upon the predicted amino acid sequence of the UT116 polypeptide consensus sequence (see Example 1). In particular, a number of UT116 peptides derived from SEQUENCE ID NO 25 were

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prepared, including the peptides of SEQUENCE ID NO 26, SEQUENCE ID NO 27, SEQUENCE ID NO 28, and SEQUENCE ID NO 29. All peptides were synthesized on a Symphony Peptide Synthesizer (available from Rainin Instrument Co, Emeryville, CA) using Fmoc chemistry, standard cycles and in-situ HBTU activation. Cleavage and deprotection conditions were as follows: a volume of 2.5 ml of cleavage reagent (77.5% v/v trifluoroacetic acid, 15% v/v ethanedithiol, 2.5% v/v water, 5% v/v thioanisole, 1-2% w/v phenol) was added to the resin, and the resulting mixture was agitated at room temperature for 2-4 hours. Then the filtrate was removed and the peptide was precipitated from the cleavage reagent with cold diethyl ether. Each peptide was filtered, purified via reverse-phase preparative HPLC using a water/acetonitrile/0.1% TFA gradient, and lyophilized. The product was confirmed by mass spectrometry.

The purified peptides were used to immunize animals (see Example 14).

Example 11a: Expression of Protein in a Cell Line Using Plasmid 577

A. Construction of a UT116 Expression Plasmid. Plasmid 577, described in U.S. patent application Serial No. 08/478,073, filed June 7, 1995 and incorporated herein by reference, has been constructed for the expression of secreted antigens in a permanent cell line. This plasmid contains the following DNA segments: (a) a 2.3 kb fragment of pBR322 containing bacterial beta-lactamase and origin of DNA replication; (b) a 1.8 kb cassette directing expression of a neomycin resistance gene under control of HSV-1 thymidine kinase promoter and poly-A addition signals; (c) a 1.9 kb cassette directing expression of a dihydrofolate reductase gene under the control of an SV-40 (Simian Virus 40) promoter and poly-A addition signals; (d) a 3.5 kb cassette directing expression of a rabbit immunoglobulin heavy chain signal sequence fused to a modified hepatitis C virus (HCV) E2 protein under the control of the SV40 T-Ag promoter and transcription enhancer, the hepatitis B virus surface antigen (HBsAg) enhancer I followed by a fragment of Herpes Simplex Virus-1 (HSV-1) genome providing poly-A addition signals; and (e) a residual 0.7 kb fragment of SV40 genome late region of no function in this plasmid. All of the segments of the vector were assembled by standard methods known to those skilled in the art of molecular biology.

Plasmids for the expression of secretable UT116 proteins are constructed by replacing the hepatitis C virus E2 protein coding sequence in plasmid 577 with that of a UT116 polynucleotide sequence selected from the group consisting of SEQUENCE ID NOS 1-12, and fragments or complements thereof, as follows. Digestion of plasmid 577 with XbaI releases the hepatitis C virus E2 gene fragment. The resulting plasmid backbone allows insertion of the UT116 cDNA insert downstream of the rabbit

immunoglobulin heavy chain signal sequence which directs the expressed proteins into the secretory pathway of the cell. The UT116 cDNA fragment is generated by PCR using standard procedures. Encoded in the sense PCR primer sequence is an XbaI site, immediately followed by a 12 nucleotide sequence that encodes the amino acid sequence Ser-Asn-Glu-Leu ("SNEL") to promote signal protease processing, efficient secretion and final product stability in culture fluids. Immediately following this 12 nucleotide sequence the primer contains nucleotides complementary to template sequences encoding amino acids of the UT116 gene. The antisense primer incorporates a sequence encoding the following eight amino acids just before the stop codons: Asp-Tyr-Lys-Asp-Asp-Asp-Lys (SEQUENCE ID NO 30). Within this sequence is incorporated a recognition site to aid in analysis and purification of the UT116 protein product. A recognition site (termed "FLAG") that is recognized by a commercially available monoclonal antibody designated anti-FLAG M2 (Eastman Kodak, Co., New Haven, CT) can be utilized, as well as other comparable sequences and their corresponding antibodies. For example, PCR is performed using GeneAmp® reagents obtained from Perkin-Elmer-Cetus, as directed by the supplier's instructions. PCR primers are used at a final concentration of 0.5 µM. PCR is performed on the UT116 plasmid template in a 100 µl reaction for 35 cycles (94°C, 30 seconds; 55°C, 30 seconds; 72°C, 90 seconds) followed by an extension cycle of 72°C for 10 min.

B. Transfection of Dihydrofolate Reductase Deficient Chinese Hamster Ovary Cells. The plasmid described *supra* is transfected into CHO/dhfr- cells [DXB-111, Uriacio et al., *PNAS* 77:4451-4466 (1980)]. These cells are available from the A.T.C.C., 12301 Parklawn Drive, Rockville, MD 20852, under Accession No. CRL 9096. Transfection is carried out using the cationic liposome-mediated procedure described by P. L. Felgner et al., *PNAS* 84:7413-7417 (1987). Particularly, CHO/dhfr- cells are cultured in Ham's F-12 media supplemented with 10% fetal calf serum, L-glutamine (1 mM) and freshly seeded into a flask at a density of 5-8 x 10<sup>5</sup> cells per flask. The cells are grown to a confluency of between 60 and 80% for transfection. Twenty micrograms (20µg) of plasmid DNA is added to 1.5 ml of Opti-MEM I medium and 100 µl of Lipofectin Reagent (Gibco-BRL; Grand Island, NY) are added to a second 1.5 ml portion of Opti-MEM I media. The two solutions are mixed and incubated at room temperature for 20 min. After the culture medium is removed from the cells, the cells are rinsed 3 times with 5 ml of Opti-MEM I medium. The Opti-MEM I-Lipofection-plasmid DNA solution then is overlaid onto the cells. The cells are incubated for 3 hr at 37°C, after which time the Opti-MEM I-Lipofectin-DNA solution is replaced with culture medium for an additional 24 hr prior to selection.

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C. Selection and Amplification. One day after transfection, cells are passaged 1:3 and incubated with dhfr/G418 selection medium (hereafter, "F-12 minus medium G"). Selection medium is Ham's F-12 with L-glutamine and without hypoxanthine, thymidine and glycine (JRH Biosciences, Lenexa, Kansas) and 300 µg per ml G418 (Gibco-BRL; Grand Island, NY). Media volume-to-surface area ratios of 5 ml per 25 cm<sup>2</sup> are maintained. After approximately two weeks, DHFR/G418 cells are expanded to allow passage and continuous maintenance in F-12 minus medium G.

Amplification of each of the transfected UT116 cDNA sequences is achieved by stepwise selection of DHFR<sup>+</sup>, G418<sup>+</sup> cells with methotrexate (reviewed by R. Schimke, Cell 37:705-713 [1984]). Cells are incubated with F-12 minus medium G containing 150 nM methotrexate (MTX) (Sigma, St. Louis, MO) for approximately two weeks until resistant colonies appear. Further gene amplification is achieved by selection of 150 nM adapted cells with 5 µM MTX.

D. Antigen Production. F-12 minus medium G supplemented with 5 µM MTX is overlaid onto just confluent monolayers for 12 to 24 hr at 37°C in 5% CO<sub>2</sub>. The growth medium is removed and the cells are rinsed 3 times with Dulbecco's phosphate buffered saline (PBS) (with calcium and magnesium) (Gibco-BRL; Grand Island, NY) to remove the remaining media/serum which may be present. Cells then are incubated with VAS custom medium (VAS custom formulation with L-glutamine with HEPES without phenol red, available from JRH Bioscience; Lenexa, KS, product number 52-08678P), for 1 hr at 37°C in 5% CO<sub>2</sub>. Cells then are overlaid with VAS for production at 5 ml per T flask. Medium is removed after seven days of incubation, retained, and then frozen to await purification with harvests 2, 3 and 4. The monolayers are overlaid with VAS for 3 more seven day harvests.

E. Analysis of Urinary Tract Tissue Gene UT116 Antigen Expression. Aliquots of VAS supernatants from the cells expressing the UT116 protein construct are analyzed, either by SDS-polyacrylamide gel electrophoresis (SDS-PAGE) using standard methods and reagents known in the art (Laemmli discontinuous gels), or by mass spectrometry.

F. Purification. Purification of the UT116 protein containing the FLAG sequence is performed by immunoaffinity chromatography using an affinity matrix comprising anti-FLAG M2 monoclonal antibody covalently attached to agarose by hydrazide linkage (Eastman Kodak Co., New Haven, CT). Prior to affinity purification, protein in pooled VAS medium harvests from roller bottles is exchanged into 50 mM Tris-HCl (pH 7.5), 150 mM NaCl buffer using a Sephadex G-25 (Pharmacia Biotech Inc., Uppsala, Sweden) column. Protein in this buffer is applied to the anti-FLAG M2 antibody affinity column. Non-binding protein is eluted by

washing the column with 50 mM Tris-HCl (pH 7.5), 150 mM NaCl buffer. Bound protein is eluted using an excess of FLAG peptide in 50 mM Tris-HCl (pH 7.5), 150 mM NaCl. The excess FLAG peptide can be removed from the purified UT116 protein by gel electrophoresis or HPLC.

5           Although plasmid 577 is utilized in this example, it is known to those skilled in the art that other comparable expression systems, such as CMV, can be utilized herein with appropriate modifications in reagent and/or techniques and are within the skill of the ordinary artisan.

10           The largest cloned insert containing the coding region of the UT116 gene is then sub-cloned into either (i) a eukaryotic expression vector which may contain, for example, a cytomegalovirus (CMV) promoter and/or protein fusible sequences which aid in protein expression and detection, or (ii) a bacterial expression vector containing a superoxide-dismutase (SOD) and CMP-KDO synthetase (CKS) or other protein fusion gene for expression of the protein sequence. Methods and vectors which are useful for  
15           the production of polypeptides which contain fusion sequences of SOD are described in EPO 0196056, published October 1, 1986, which is incorporated herein by reference and those containing fusion sequences of CKS are described in EPO Publication No. 0331961, published September 13, 1989, which publication is also incorporated herein by reference. This so-purified protein can be used in a variety of techniques,  
20           including, but not limited to animal immunization studies, solid phase immunoassays, etc.

Example 11b: Expression of Protein in a Cell Line Using pcDNA3.1/Myc-His

25           A. Construction of a UT116 Expression Plasmid. Plasmid pcDNA3.1/Myc-His (Cat.# V855-20, Invitrogen, Carlsbad, CA) has been constructed, in the past, for the expression of secreted antigens by most mammalian cell lines. Expressed protein inserts are fused to a myc-his peptide tag. The myc-his tag is a 21 residue amino acid sequence having the following sequence: Glu-Gln-Lys-Leu-Ile-Ser-Glu- Glu-Asp-Leu-Asn-Met-His-Thr-Glu-His-His-His-His-His (SEQUENCE ID NO 31) and  
30           comprises a c-myc oncoprotein epitope and a polyhistidine sequence which are useful for the purification of an expressed fusion protein by using either anti-myc or anti-his affinity columns, or metalloprotein binding columns.

35           A plasmid for the expression of secretable UT116 proteins is constructed by inserting a UT116 polynucleotide sequence from clone 1543671 into the pcDNA3.1/Myc-His vector. (This plasmid will be hereinafter referred to as pc1543671-M/H.) Prior to construction of pc1543671-M/H, the UT116 cDNA sequence is first cloned into a pCR<sup>®</sup>-Blunt vector as follows.

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The UT116 cDNA fragment is generated by PCR using standard procedures. For example, PCR is performed using Stratagene® reagents obtained from Stratagene, as directed by the manufacturer's instructions. PCR primers are used at a final concentration of 0.5 µM. PCR using 5 U of pfu polymerase (Stratagene, La Jolla, CA) is performed on the UT116 plasmid template (see Example 2) in a 50 µl reaction for 30 cycles (94°C, 1 min; 65°C, 1.5 min; 72°C, 3 min) followed by an extension cycle of 72°C for 10 min. The sense PCR primer sequence is identical to that found directly upstream of the UT116 insertion site in the pINCY vector. The antisense PCR primer sequence incorporates a 5' NotI restriction sequence and a sequence complementary to the 3' end of the UT116 directly upstream of the 3'-most in-frame stop codon. Five microliters (5 µl) of the resulting blunted-ended PCR product are ligated into 25 ng of linearized pCR<sup>+</sup>-Blunt vector (Invitrogen, Carlsbad, CA) interrupting the lethal ccdB gene of the vector. The resulting ligated vector is transformed into TOP10 *E. coli* (Invitrogen, Carlsbad, CA) using a One Shot™ transformation kit (Invitrogen, Carlsbad, CA) following manufacturer's directions. The transformed cells are grown on LB-Kan (50 µg/ml kanamycin) selection plates at 37°C. Only cells containing a plasmid with an interrupted ccdB gene will grow after transformation [Grant, S.G.N., PNAS 87:4645-4649 (1990)]. Transformed colonies are picked and grown up in 3 ml of LB-Kan broth at 37°C. Plasmid DNA is isolated by using a QIAprep® (Qiagen Inc., Santa Clarita, CA) procedure, as directed by the manufacturer. The DNA is digested with EcoRI or SnaBI, and NotI restriction enzymes to release the UT116 insert fragment. The fragment is electrophoresed on 1% Seakem® LE agarose/0.5 µg/ml ethidium bromide/TE gel, visualized by UV irradiation, excised and purified using QIAquick™ (Qiagen Inc., Santa Clarita, CA) procedures, as directed by the manufacturer.

The pcDNA3.1/Myc-His plasmid DNA is linearized by digestion with EcoRI and NotI in the polylinker region of the plasmid DNA. The purified UT116 fragment is ligated with the resulting plasmid DNA backbone, downstream of a CMV promoter which directs expression of the proteins in mammalian cells. The ligated plasmid is transformed into DH5α™ cells (GibcoBRL Grand Island, NY), as directed by the manufacturer. Briefly, 10 ng of pcDNA3.1/Myc-His containing a UT116 insert are added to 50 µl of competent DH5 alpha cells, and the contents are mixed gently. The mixture is incubated on ice for 30 min, heat shocked for 20 sec at 37°C, and placed on ice for an additional 2 min. Upon addition of 0.95 ml of LB medium, the mixture is incubated for 1 hr at 37°C while shaking at 225 rpm. The transformed cells then are plated onto 100 mm LB/ampicillin (50µg/ml) plates and grown at 37°C. Colonies are picked and grown in 3 ml of LB/ ampicillin broth. Plasmid DNA is purified using a

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QIAprep kit (Qiagen Inc., Santa Clarita, CA). The presence of the insert is confirmed using techniques known to those skilled in the art, including, but not limited to restriction digestion and gel analysis. (J. Sambrook et al., supra.)

- 5        B. Transfection of Human Embryonic Kidney Cell 293 Cells. The UT116 expression plasmid described in section A, supra, is retransformed into DH5 $\alpha$ <sup>TM</sup> cells, plated onto LB/ampicillin agar, and grown up in 10 ml of LB/ampicillin broth, as described hereinabove. The plasmid is purified using a QIAfilter<sup>TM</sup> Maxi kit (Qiagen, Chatsworth, CA) and is transfected into HEK293 cells [F.L. Graham et al., J. Gen. Vir. 36:59-72 (1977)]. These cells are available from the A.T.C.C., 12301 Parklawn Drive, Rockville, MD 20852, under Accession No. CRL 1573. Transfection is carried out using the cationic lipofectamine-mediated procedure described by P. Hawley-Nelson et al., Focus 15.73 (1993). Particularly, HEK293 cells are cultured in 10 ml DMEM media supplemented with 10% fetal bovine serum (FBS), L-glutamine (2 mM) and freshly seeded into 100 mm culture plates at a density of  $9 \times 10^6$  cells per plate.
- 10       The cells are grown at 37 °C to a confluency of between 70% and 80% for transfection. Eight micrograms (8  $\mu$ g) of plasmid DNA are added to 800  $\mu$ l of Opti-MEM I<sup>®</sup> medium (Gibco-BRL, Grand Island, NY), and 48-96  $\mu$ l of Lipofectamine<sup>TM</sup> Reagent (Gibco-BRL, Grand Island, NY) are added to a second 800  $\mu$ l portion of Opti-MEM I media. The two solutions are mixed and incubated at room temperature for 15-30 min.
- 15       After the culture medium is removed from the cells, the cells are washed once with 10 ml of serum-free DMEM. The Opti-MEM I-Lipofectamine-plasmid DNA solution is diluted with 6.4 ml of serum-free DMEM and then overlaid onto the cells. The cells are incubated for 5 hr at 37°C, after which time, an additional 8 ml of DMEM with 20% FBS are added. After 18-24 hr, the old medium is aspirated, and the cells are overlaid
- 20       with 5 ml of fresh DMEM with 5% FBS. Supernatants and cell extracts are analyzed for UT116 gene activity 72 hr after transfection.

- C. Analysis of Urinary Tract Tissue Gene UT116 Antigen Expression. The culture supernatant, supra, is transferred to cryotubes and stored on ice. HEK293 cells are harvested by washing twice with 10 ml of cold Dulbecco's PBS and lysing by
- 30       addition of 1.5 ml of CAT lysis buffer (Boehringer Mannheim, Indianapolis, IN), followed by incubation for 30 min at room temperature. Lysate is transferred to 1.7 ml polypropylene microfuge tubes and centrifuged at 1000 x g for 10 min. The supernatant is transferred to new cryotubes and stored on ice. Aliquots of supernatants from the cells and the lysate of the cells expressing the UT116 protein construct are
- 35       analyzed for the presence of UT116 recombinant protein.

The aliquots are run on SDS-polyacrylamide gel electrophoresis (SDS-PAGE) using standard methods and reagents known in the art. (J. Sambrook et al., supra). For

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SDS-PAGE, samples are mixed with an equal volume of 2X Tricine sample buffer (Novex, San Diego, CA) and heated for 5 minutes at 100°C. Samples are then applied to a Novex 10-20% Precast Tricine Gel for electrophoresis. Following electrophoresis, samples are transferred from the gels to nitrocellulose membranes in Novex Tris-Glycine Transfer buffer. Membranes are then probed with an anti-myc epitope monoclonal antibody (Invitrogen, Carlsbad, CA) followed by the reagents and procedures provided in the Western Lights Plus or Western Lights detection kits (Tropix, Bedford, MA). These probed membranes are then treated with biotinylated goat-antimouse or biotinylated goat-antirabbit antibody and Avidex streptavidin-alkaline phosphatase conjugate (both from Tropix, Bedford, MA). Final treatment of the blot with the chemiluminescent substrate CSPD (Tropix, Bedford, MA) and exposure to photographic film (Hyperfilm ECL Amersham, Buckinghamshire, England) visualizes the bands.

Alternatively, the expressed UT116 recombinant protein can be analyzed by mass spectrometry (see Example 12).

D. Purification. Purification of the UT116 recombinant protein containing the myc-his sequence is performed using the Xpress® affinity chromatography system (Invitrogen, Carlsbad, CA) containing a nickel-charged agarose resin which specifically binds polyhistidine residues. Supernatants from 10x100 mm plates, prepared as described supra, are pooled and passed over the nickel-charged column. Non-binding protein is eluted by washing the column with 50 mM Tris-HCl (pH 7.5)/150 mM NaCl buffer, leaving only the myc-his fusion proteins. Bound UT116 recombinant protein then is eluted from the column using either an excess of imidazole or histidine, or a low pH buffer. Alternatively, the recombinant protein can also be purified by binding at the myc-his sequence to an affinity column consisting of either anti-myc or anti-histidine monoclonal antibodies conjugated through a hydrazide or other linkage to an agarose resin and eluting with an excess of myc peptide or histidine, respectively.

The purified recombinant protein can then be covalently cross-linked to a solid phase, such as N-hydroxysuccinimide-activated sepharose columns (Pharmacia Biotech, Piscataway, NJ), as directed by supplier's instructions. These columns containing covalently linked UT116 recombinant protein, can then be used to purify anti-UT116 antibodies from rabbit or mouse sera (see Examples 13 and 14).

E. Coating Microtiter Plates with UT116 Expressed Proteins. Supernatant from a 100 mm plate, as described supra, is diluted in an appropriate volume of PBS. Then, 100 µl of the resulting mixture are placed into each well of a Reacti-Bind™ metal chelate microtiter plate (Pierce, Rockford, IL), incubated at room temperature while

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shaking, and followed by three washes with 200 µl each of PBS with 0.05% Tween® 20. The prepared microtiter plate can then be used to screen polyclonal antisera for the presence of UT116 antibodies (see Example 17).

Although pcDNA3.1/Myc-His is utilized in this example, it is known to those skilled in the art that other comparable expression systems can be utilized herein with appropriate modifications in reagent and/or techniques and are within the skill of one of ordinary skill in the art. The largest cloned insert containing the coding region of the UT116 gene is sub-cloned into either (i) a eukaryotic expression vector which may contain, for example, a cytomegalovirus (CMV) promoter and/or protein fusible sequences which aid in protein expression and detection, or (ii) a bacterial expression vector containing a superoxide-dismutase (SOD) and CMP-KDO synthetase (CKS) or other protein fusion gene for expression of the protein sequence. Methods and vectors which are useful for the production of polypeptides which contain fusion sequences of SOD are described in published EPO application No. EP 0 196 056, published October 1, 1986, which is incorporated herein by reference, and vectors containing fusion sequences of CKS are described in published EPO application No. EP 0 331 961, published September 13, 1989, which publication is also incorporated herein by reference. The purified protein can be used in a variety of techniques, including, but not limited to animal immunization studies, solid phase immunoassays, etc.

#### Example 12: Chemical Analysis of Urinary Tract Tissue Proteins

A. Analysis of Tryptic Peptide Fragments Using MS. Sera from patients with urinary tract disease, such as urinary tract cancer, sera from patients with no urinary tract disease, extracts of urinary tract tissues or cells from patients with urinary tract disease, such as urinary tract cancer, extracts of urinary tract tissues or cells from patients with no urinary tract disease, and extracts of tissues or cells from other non-diseased or diseased organs of patients, are run on a polyacrylamide gel using standard procedures and stained with Coomassie Blue. Sections of the gel suspected of containing the unknown polypeptide are excised and subjected to an in-gel reduction, acetamidation and tryptic digestion. P. Jeno et al, Anal. Bio. 224:451-455 (1995) and J. Rosenfeld et al, Anal. Bio. 203:173-179 (1992). The gel sections are washed with 100 mM NH<sub>4</sub>HCO<sub>3</sub> and acetonitrile. The shrunken gel pieces are swollen in digestion buffer (50 mM NH<sub>4</sub>HCO<sub>3</sub>, 5 mM CaCl<sub>2</sub> and 12.5 µg/ml trypsin) at 4°C for 45 min. The supernatant is aspirated and replaced with 5 to 10 µl of digestion buffer without trypsin and allowed to incubate overnight at 37°C. Peptides are extracted with 3 changes of 5% formic acid and acetonitrile and evaporated to dryness. The peptides are adsorbed to approximately 0.1 µl of POROS R2 sorbent (Perseptive Biosystems,

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Framingham, Massachusetts) trapped in the tip of a drawn gas chromatography capillary tube by dissolving them in 10 µl of 5% formic acid and passing it through the capillary. The adsorbed peptides are washed with water and eluted with 5% formic acid in 60% methanol. The eluant is passed directly into the spraying capillary of an

5 API III mass spectrometer (Perkin-Elmer Sciex, Thornhill, Ontario, Canada) for analysis by nano-electrospray mass spectrometry. M. Wilm et al., Int. J. Mass Spectrom. Ion Process 136:167-180 (1994) and M. Wilm et al., Anal. Chem. 66:1-8 (1994). The masses of the tryptic peptides are determined from the mass spectrum obtained off the first quadrupole. Masses corresponding to predicted peptides can be

10 further analyzed in MS/MS mode to give the amino acid sequence of the peptide.

B. Peptide Fragment Analysis Using LC/MS. The presence of polypeptides predicted from mRNA sequences found in hyperplastic disease tissues also can be confirmed using liquid chromatography/tandem mass spectrometry (LC/MS/MS). D. Hess et al., METHODS, A Companion to Methods in Enzymology 6:227-238 (1994).

15 The serum specimen or tumor extract from the patient is denatured with SDS and reduced with dithiothreitol (1.5 mg/ml) for 30 min at 90°C followed by alkylation with iodoacetamide (4 mg/ml) for 15 min at 25°C. Following acrylamide electrophoresis, the polypeptides are electroblotted to a cationic membrane and stained with Coomassie Blue. Following staining, the membranes are washed and sections thought to contain

20 the unknown polypeptides are cut out and dissected into small pieces. The membranes are placed in 500 µl microcentrifuge tubes and immersed in 10 to 20 µl of proteolytic digestion buffer (100 mM Tris-HCl, pH 8.2, containing 0.1 M NaCl, 10% acetonitrile, 2 mM CaCl<sub>2</sub> and 5 µg/ml trypsin) (Sigma, St. Louis, MO). After 15 hr at 37°C, 3 µl of saturated urea and 1 µl of 100 µg/ml trypsin are added and incubated for an

25 additional 5 hr at 37°C. The digestion mixture is acidified with 3 µl of 10% trifluoroacetic acid and centrifuged to separate supernatant from membrane. The supernatant is injected directly onto a microbore, reverse phase HPLC column and eluted with a linear gradient of acetonitrile in 0.05% trifluoroacetic acid. The eluate is fed directly into an electrospray mass spectrometer, after passing though a stream

30 splitter if necessary to adjust the volume of material. The data is analyzed following the procedures set forth in Example 12, Section A.

#### Example 13: Gene Immunization Protocol

35 A. In Vivo Antigen Expression. Gene immunization circumvents protein purification steps by directly expressing an antigen in vivo after inoculation of the appropriate expression vector. Also, production of antigen by this method may allow correct protein folding and glycosylation since the protein is produced in mammalian

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not conjugated to a carrier such as keyhole limpet hemocyanine, KLH, (i.e., they were unconjugated.).

Female white New Zealand rabbits weighing 2 kg or more were used for raising polyclonal antiserum. One animal was immunized per unconjugated peptide (SEQUENCE ID NO 26, SEQUENCE ID NO 27, or SEQUENCE ID NO 28). One week prior to the first immunization, a 5 to 10 ml sample of blood was obtained from each animal to serve as a non-immune prebleed sample.

Unconjugated peptides, SEQUENCE ID NO 26, SEQUENCE ID NO 27, and SEQUENCE ID NO 28, were used to prepare the primary immunogen by emulsifying 0.5 ml of the peptide at a concentration of 2 mg/ml in PBS (pH 7.2) which contained 0.5 ml of complete Freund's adjuvant (CFA) (Difco, Detroit, MI). The immunogen was injected into several sites of the animal via subcutaneous, intraperitoneal, and intramuscular routes of administration. Four weeks following the primary immunization, a booster immunization was administered. The immunogen used for the booster immunization dose was prepared by emulsifying 0.5 ml of the same unconjugated peptide used for the primary immunogen, except that the peptide now was diluted to 1 mg/ml with 0.5 ml of incomplete Freund's adjuvant (IFA) (Difco, Detroit, MI). Again, the booster dose was administered into several sites via subcutaneous, intraperitoneal and intramuscular types of injections. The animals were bled (5 ml) two weeks after the booster immunizations and each serum was tested for immunoreactivity to the peptide as described below. The booster and bleed schedule was repeated at 4 week intervals until an adequate titer was obtained. The titer or concentration of antiserum was determined by using unconjugated peptides in a microtiter EIA as described in Example 17, below. An antibody titer of 1:500 or greater was considered an adequate titer for further use and study.

Table 2. Titer of rabbit anti-UT116 peptide antisera (11 week bleed)

<u>Peptide Immunogen</u>	<u>Titer</u>
SEQUENCE ID NO 26	141,000
SEQUENCE ID NO 27	46,000
SEQUENCE ID NO 28	19,000

#### 30 B. Production of Monoclonal Antibody.

1. Immunization Protocol. Mice are immunized using peptides which can either be conjugated to a carrier such as KLH [prepared as described hereinbelow, or unconjugated (i.e., not conjugated to a carrier such as KLH)] except that the amount

of the unconjugated or conjugated peptide for monoclonal antibody production in mice is one-tenth the amount used to produce polyclonal antisera in rabbits. Thus, the primary immunogen consists of 100 µg of unconjugated or conjugated peptide in 0.1 ml of CFA emulsion while the immunogen used for booster immunizations consists of 50 µg of unconjugated or conjugated peptide in 0.1 ml of IFA. Hybridomas for the generation of monoclonal antibodies are prepared and screened using standard techniques. The methods used for monoclonal antibody development follow procedures known in the art such as those detailed in Kohler and Milstein, Nature 256:494 (1975) and reviewed in J.G.R. Hurrel, ed., Monoclonal Hybridoma Antibodies: Techniques and Applications, CRC Press, Inc., Boca Raton, FL (1982). Another method of monoclonal antibody development which is based on the Kohler and Milstein method is that of L.T. Mimms et al., Virology 176:604-619 (1990), which is incorporated herein by reference.

The immunization regimen (per mouse) consists of a primary immunization with additional booster immunizations. The primary immunogen used for the primary immunization consists of 100 µg of unconjugated or conjugated peptide in 50 µl of PBS (pH 7.2) previously emulsified in 50 µl of CFA. Booster immunizations performed at approximately two weeks and four weeks post primary immunization consist of 50 µg of unconjugated or conjugated peptide in 50 µl of PBS (pH 7.2) emulsified with 50 µl IFA. A total of 100 µl of this immunogen are inoculated intraperitoneally and subcutaneously into each mouse. Individual mice are screened for immune response by microtiter plate enzyme immunoassay (EIA) as described in Example 17 approximately four weeks after the third immunization. Mice are inoculated either intravenously, intrasplenically or intraperitoneally with 50 µg of unconjugated or conjugated peptide in PBS (pH 7.2) approximately fifteen weeks after the third immunization..

Three days after this intravenous boost, splenocytes are fused with, for example, Sp2/0-Ag14 myeloma cells (Milstein Laboratories, England) using the polyethylene glycol (PEG) method. The fusions are cultured in Iscove's Modified Dulbecco's Medium (IMDM) containing 10% fetal calf serum (FCS), plus 1% hypoxanthine, aminopterin and thymidine (HAT). Bulk cultures are screened by microtiter plate EIA following the protocol in Example 17. Clones reactive with the peptide used as an immunogen and non-reactive with other peptides (i.e., peptides of UT116 not used as the immunogen) are selected for final expansion. Clones thus selected are expanded, aliquoted and frozen in IMDM containing 10% FCS and 10% dimethyl sulfoxide (DMSO).

2. Peptide Conjugation. Peptide is conjugated to maleimide activated KLH (commercially available as Imject®, available from Pierce Chemical Company, Rockford, IL). Imject® contains about 250 moles of reactive maleimide groups per mole of hemocyanine. The activated KLH is dissolved in phosphate buffered saline (PBS, pH 8.4) at a concentration of about 7.7 mg/ml. The peptide is conjugated through cysteines occurring in the peptide sequence, or to a cysteine previously added to the synthesized peptide in order to provide a point of attachment. The peptide is dissolved in DMSO (Sigma Chemical Company, St. Louis, MO) and reacted with the activated KLH at a mole ratio of about 1.5 moles of peptide per mole of reactive maleimide attached to the KLH. A procedure for the conjugation of peptide is provided hereinbelow. It is known to the ordinary artisan that the amounts, times and conditions of such a procedure can be varied to optimize peptide conjugation.

The conjugation reaction described hereinbelow is based on obtaining 3 mg of KLH peptide conjugate ("conjugated peptide"), which contains about 0.77 µmoles of reactive maleimide groups. This quantity of peptide conjugate usually is adequate for one primary injection and four booster injections for production of polyclonal antisera in a rabbit. Briefly, peptide is dissolved in DMSO at a concentration of 1.16 µmoles/100 µl of DMSO. One hundred microliters (100 µl) of the DMSO solution are added to 380 µl of the activated KLH solution prepared as described hereinabove, and 20 µl of PBS (pH 8.4) are added to bring the volume to 500 µl. The reaction is incubated overnight at room temperature with stirring. The extent of reaction is determined by measuring the amount of unreacted thiol in the reaction mixture. The difference between the starting concentration of thiol and the final concentration is assumed to be the concentration of peptide which has coupled to the activated KLH. The amount of remaining thiol is measured using Ellman's reagent (5,5'-dithiobis(2-nitrobenzoic acid), Pierce Chemical Company, Rockford, IL). A series of cysteine standards is made at concentrations of 0, 0.1, 0.5, 2, 5 and 20 mM by dissolving 35 mg of cysteine HCl (Pierce Chemical Company, Rockford, IL) in 10 ml of PBS (pH 7.2) and diluting the stock solution to the desired concentrations. The photometric determination of the concentration of thiol is accomplished by placing 200 µl of PBS (pH 8.4) in each well of an Immulon 2® microwell plate (Dynex Technologies, Chantilly, VA). Next, 10 µl of standard or reaction mixture are added to each well. Finally, 20 µl of Ellman's reagent at a concentration of 1 mg/ml in PBS (pH 8.4) are added to each well. The wells are incubated for 10 minutes at room temperature, and the absorbance of all wells is read at 415 nm with a microplate reader (such as the BioRad Model 3550, BioRad, Richmond, CA). The absorbance of the standards is used to construct a standard curve and the thiol concentration of the

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B65750-42862060

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reaction mixture is determined from the standard curve. A decrease in the concentration of free thiol is indicative of a successful conjugation reaction. Unreacted peptide is removed by dialysis against PBS (pH 7.2) at room temperature for 6 hours. The conjugate is stored at 2-8°C if it is to be used immediately; otherwise, it is stored at -20°C or colder.

3. Production of Ascites Fluid Containing Monoclonal Antibodies.

Frozen hybridoma cells prepared as described hereinabove are thawed and placed into expansion culture. Viable hybridoma cells are inoculated intraperitoneally into Pristane treated mice. Ascitic fluid is removed from the mice, pooled, filtered through a 0.2 µ filter and subjected to an immunoglobulin class G (IgG) analysis to determine the volume of the Protein A column required for the purification.

4. Purification of Monoclonal Antibodies From Ascites Fluid. Briefly,

filtered and thawed ascites fluid is mixed with an equal volume of Protein A sepharose binding buffer (1.5 M glycine, 3.0 M NaCl, pH 8.9) and refiltered through a 0.2 µ filter. The volume of the Protein A column is determined by the quantity of IgG present in the ascites fluid. The eluate then is dialyzed against PBS (pH 7.2) overnight at 2-8°C. The dialyzed monoclonal antibody is sterile filtered and dispensed in aliquots. The immunoreactivity of the purified monoclonal antibody is confirmed by determining its ability to specifically bind to the peptide used as the immunogen by use of the EIA microtiter plate assay procedure of Example 17. The specificity of the purified monoclonal antibody is confirmed by determining its lack of binding to irrelevant peptides such as peptides of UT116 not used as the immunogen. The purified anti-UT116 monoclonal thus prepared and characterized is placed at either 2-8°C for short term storage or at -80°C for long term storage.

5. Further Characterization of Monoclonal Antibody. The isotype and

subtype of the monoclonal antibody produced as described hereinabove can be determined using commercially available kits (available from Amersham. Inc., Arlington Heights, IL). Stability testing also can be performed on the monoclonal antibody by placing an aliquot of the monoclonal antibody in continuous storage at 2-8°C and assaying optical density (OD) readings throughout the course of a given period of time.

C. Use of Recombinant Proteins as Immunogens. It is within the scope of the

present invention that recombinant proteins made as described herein can be utilized as immunogens in the production of polyclonal and monoclonal antibodies, with corresponding changes in reagents and techniques known to those skilled in the art.



Example 15: Purification of Serum Antibodies Which Specifically  
Bind to UT116 Peptides

Immune sera, obtained as described hereinabove in Examples 13 and/or 14, is affinity purified using immobilized synthetic peptides prepared as described in Example 10, or recombinant proteins prepared as described in Example 11. An IgG fraction of the antiserum is obtained by passing the diluted, crude antiserum over a Protein A column (Affi-Gel protein A, Bio-Rad, Hercules, CA). Elution with a buffer (Binding Buffer, supplied by the manufacturer) removes substantially all proteins that are not immunoglobulins. Elution with 0.1 M buffered glycine (pH 3) gives an immunoglobulin preparation that is substantially free of albumin and other serum proteins.

Immunoaffinity chromatography is performed to obtain a preparation with a higher fraction of specific antigen-binding antibody. The peptide used to raise the antiserum is immobilized on a chromatography resin, and the specific antibodies directed against its epitopes are adsorbed to the resin. After washing away non-binding components, the specific antibodies are eluted with 0.1 M glycine buffer, pH 2.3. Antibody fractions are immediately neutralized with 1.0 M Tris buffer (pH 8.0) to preserve immunoreactivity. The chromatography resin chosen depends on the reactive groups present in the peptide. If the peptide has an amino group, a resin such as Affi-Gel 10 or Affi-Gel 15 is used (Bio-Rad, Hercules, CA). If coupling through a carboxy group on the peptide is desired, Affi-Gel 102 can be used (Bio-Rad, Hercules, CA). If the peptide has a free sulfhydryl group, an organomercurial resin such as Affi-Gel 501 can be used (Bio-Rad, Hercules, CA).

Alternatively, spleens can be harvested and used in the production of hybridomas to produce monoclonal antibodies following routine methods known in the art as described hereinabove.

Example 16: Western Blotting of Tissue Samples

Protein extracts were prepared by homogenizing tissue samples in 0.1M Tris-HCl (pH 7.5), 15% (w/v) glycerol, 0.2 mM EDTA, 1.0 mM 1,4-dithiothreitol, 10 µg/ml leupeptin and 1.0 mM phenylmethylsulfonylfluoride [S. R. Kain et al., Biotechniques 17:982 (1994)]. Following homogenization, the homogenates were centrifuged at 4°C for 20 minutes to separate supernatant from debris. The debris was re-extracted by homogenization with a buffer that was similar to above but also contained 0.1 M Tricine and 0.1% SDS. The supernate from the second extraction was used for Western blotting. For protein quantitation, 2-5 µl of supernate were added to

-80-

1.5 ml of Coomassie Protein Reagent (Pierce, Rockford, IL) and the absorbance was read at 595 nm.

For SDS-PAGE, samples were adjusted to desired protein concentration with Tricine Buffer (Novex, San Diego, CA), mixed with an equal volume of 2X Tricine sample buffer (Novex, San Diego, CA), and heated for 5 minutes at 100°C in a thermal  
5 cycler. Samples were then applied to a Novex 10-20% Precast Tricine Gel for electrophoresis. Following electrophoresis, samples were transferred from the gels to nitrocellulose membranes in Novex Tris-Glycine Transfer buffer. Membranes were then probed with specific anti-peptide antibodies using the reagents and procedures  
10 provided in the Western Lights or Western Lights Plus (Tropix, Bedford, MA) chemiluminescence detection kits. Chemiluminescent bands were visualized by exposing the developed membranes to Hyperfilm ECL (Amersham, Arlington Heights, IL).

Figure 4 shows the results of the Western blot performed on a panel of tissue extracts using antiserum against UT116 synthetic peptide (SEQUENCE ID NO 27; see  
15 Example 14). Each lane of Figure 4 represents a different tissue protein extract: (1) bladder cancer; (2) normal bladder; (3) bladder cancer; (4) normal bladder; (5) bladder cancer; (6) normal colon; (7) normal lung; (8) normal breast; (9-11) prostate cancer; (12) BPH; and (13) markers. A broad band between 31 and 45 kD is seen with the bladder cancer sample shown in lane 3. A sharper band above 31 kD is seen with a  
20 prostate cancer sample (lane 10) and to a lesser extent with a BPH sample (lane 12).

Competition experiments were performed in an analogous manner as above with the single exception that the primary antibodies against UT116 synthetic peptide (SEQUENCE ID NO 27) were pre-incubated overnight at 4°C with varying  
25 concentrations of peptide immunogen prior to exposure to the nitrocellulose filter. Development of the Westerns was continued as above. Antibody binding to the broad band seen with the bladder cancer sample (lane 3) was inhibited at a saturating concentration of synthetic peptide (SEQUENCE ID NO 27).

After visualization of the bands on film, the bands were also visualized directly on the membranes by the addition and development of chromogenic substrate 5-bromo-  
30 4-chloro-3-indolyl phosphate (BCIP). This chromogenic solution contains 0.016% BCIP in a solution containing 100 mM NaCl, 5 mM MgCl<sub>2</sub> and 100 mM Tris-HCl, pH 9.5. The filter was incubated in the solution at room temperature until the bands developed to the desired intensity. Molecular mass determination was made based upon the mobility of pre-stained molecular weight standards (Novex, San Diego, CA)  
35 and biotinylated molecular weight standards (Tropix, Bedford, MA).

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Example 17: EIA Microtiter Plate Assay

The immunoreactivity of antiserum preferably obtained from rabbits or mice as described in Example 13 or Example 14 was determined by means of a microtiter plate EIA, as follows. Briefly, the synthetic UT116 peptides of SEQUENCE ID NO 26, SEQUENCE ID NO 27, and SEQUENCE ID NO 28 (prepared as described in Example 10) were dissolved in carbonate buffer (50 mM, pH 9.6) to a final concentration of 2 µg/ml. Next, 100 µl of the peptide or protein solution were placed in each well of an Immulon 2® microtiter plate (Dynex Technologies, Chantilly, VA). The plate was incubated overnight at room temperature and then washed four times with deionized water. The wells were blocked by adding 125 µl of a suitable protein blocking agent, such as Superblock® (Pierce Chemical Company, Rockford, IL), to each well and then immediately discarding the solution. This blocking procedure was performed three times. Antiserum obtained from immunized rabbits or mice, prepared as previously described, was diluted in a protein blocking agent (e.g., a 3% Superblock® solution) in PBS containing 0.05% Tween-20® [(monolaurate polyoxyethylene ether) (Sigma Chemical Company, St. Louis, MO)] and 0.05% sodium azide at dilutions of 1:100, 1:500, 1:2500, 1:12,500, and 1:62,500 and placed in each well of the coated microtiter plate. The wells then were incubated for three hours at room temperature. Each well was washed four times with deionized water. One hundred microliters of alkaline phosphatase-conjugated goat anti-rabbit IgG or goat anti-mouse IgG antiserum (Southern Biotech, Birmingham, AB) diluted 1:2000 in 3% Superblock® solution in phosphate buffered saline containing 0.05% Tween 20® and 0.05% sodium azide, were added to each well. The wells were incubated for two hours at room temperature. Next, each well was washed four times with deionized water. One hundred microliters of paranitrophenyl phosphate substrate (Kirkegaard and Perry Laboratories, Gaithersburg, MD) then were added to each well. The wells were incubated for thirty minutes at room temperature. The absorbance at 405 nm was read in each well. Positive reactions were identified by an increase in absorbance at 405 nm in the test well above that absorbance given by a non-immune serum (negative control). A positive reaction was indicative of the presence of detectable anti-UT116 antibodies. Titers of the anti-peptide antisera were calculated from the previously described dilutions of antisera and defined as the calculated dilution, where  $A_{405nm}=0.5$  OD.

Example 18: Coating of Solid Phase Particles

A. Coating of Microparticles with Antibodies Which Specifically Bind to UT116 Antigen. Affinity purified antibodies which specifically bind to UT116 protein

5 ethylcarbodiimide hydrochloride (Aldrich Chemical Co., Milwaukee, WI) activated  
carboxylated latex microparticles with antibodies which specifically bind to UT116  
protein, as follows. Briefly, a final 0.375% solid suspension of resin washed  
carboxylated latex microparticles (available from Bangs Laboratories, Carmel, IN or  
Serodyn, Indianapolis, IN) are mixed in a solution containing 50 mM MES buffer, pH  
10 4.0 and 150 mg/l of affinity purified anti-UT116 antibody (see Example 14) for 15 min  
in an appropriate container. EDAC coupling agent is added to a final concentration of  
5.5  $\mu\text{g/ml}$  to the mixture and mixed for 2.5 hr at room temperature.

15     Filtration module. Washed microparticles are stored in an appropriate buffer which usually contains a dilute surfactant and irrelevant protein as a blocking agent, until needed.

20 methods known in the art (Snitman et al, US Patent 5,273,882, incorporated herein by reference) and used in competitive binding or EIA sandwich assays.

25 10 mM carbonate buffer, pH 8 to 9.5. The antibody solution can be as dilute as 1  
μg/ml in the case of high affinity monoclonal antibodies or as concentrated as about  
500 μg/ml for polyclonal antibodies which have not been affinity purified. Beads are  
coated for at least 12 hours at room temperature, and then they are washed with  
deionized water. Beads may be air dried or stored wet (in PBS, pH 7.4). They also  
30 may be overcoated with protein stabilizers (such as sucrose) or protein blocking agents  
used as non-specific binding blockers (such as irrelevant proteins, Carnation skim  
milk, Superblock®, or the like).

### Example 19: Microparticle Enzyme Immunoassay (MEIA)

35 UT116 antigens are detected in patient test samples by performing a standard antigen competition EIA or antibody sandwich EIA and utilizing a solid phase such as

microparticles (MEIA). The assay can be performed on an automated analyzer such as the IMx<sup>®</sup> Analyzer (Abbott Laboratories, Abbott Park, IL).

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A. Antibody Sandwich EIA. Briefly, samples suspected of containing UT116 antigen are incubated in the presence of anti-UT116 antibody-coated microparticles (prepared as described in Example 17) in order to form antigen/antibody complexes. The microparticles then are washed and an indicator reagent comprising an antibody conjugated to a signal generating compound (i.e., enzymes such as alkaline phosphatase or horseradish peroxide) is added to the antigen/antibody complexes or the microparticles and incubated. The microparticles are washed and the bound antibody/antigen/antibody complexes are detected by adding a substrate (e.g., 4-methylumbelliferyl phosphate (MUP), or OPD/peroxide, respectively), that reacts with the signal generating compound to generate a measurable signal. An elevated signal in the test sample, compared to the signal generated by a negative control, detects the presence of UT116 antigen. The presence of UT116 antigen in the test sample is indicative of a diagnosis of a urinary tract disease or condition, such as urinary tract cancer.

B. Competitive Binding Assay. The competitive binding assay uses a peptide or protein that generates a measurable signal when the labeled peptide is contacted with an anti-peptide antibody coated microparticle. This assay can be performed on the IMx<sup>®</sup> Analyzer (available from Abbott Laboratories, Abbott Park, IL). The labeled peptide is added to the UT116 antibody-coated microparticles (prepared as described in Example 17) in the presence of a test sample suspected of containing UT116 antigen, and incubated for a time and under conditions sufficient to form labeled UT116 peptide (or labeled protein) / bound antibody complexes and/or patient UT116 antigen / bound antibody complexes. The UT116 antigen in the test sample competes with the labeled UT116 peptide (or UT116 protein) for binding sites on the microparticle. UT116 antigen in the test sample results in a lowered binding of labeled peptide and antibody coated microparticles in the assay since antigen in the test sample and the UT116 peptide or UT116 protein compete for antibody binding sites. A lowered signal (compared to a control) indicates the presence of UT116 antigen in the test sample. The presence of UT116 antigen suggests the diagnosis of a urinary tract disease or condition, such as urinary tract cancer.

The UT116 polynucleotides and the proteins encoded thereby which are provided and discussed hereinabove are useful as markers of urinary tract tissue disease, especially urinary tract cancer. Tests based upon the appearance of this marker in a test sample such as blood, plasma or serum can provide low cost, non-invasive, diagnostic information to aid the physician to make a diagnosis of cancer, to help select

a therapy protocol, or to monitor the success of a chosen therapy. This marker may appear in readily accessible body fluids such as blood, urine or stool as antigens derived from the diseased tissue which are detectable by immunological methods. This marker may be elevated in a disease state, altered in a disease state, or be a normal protein of the urinary tract which appears in an inappropriate body compartment.

Example 20: Immunohistochemical Detection of UT116 Protein

Antiserum against SEQUENCE ID NO 27 described in Example 14, above, was used to immunohistochemically stain a variety of normal and diseased tissues using standard procedures. Briefly, frozen blocks of tissue were cut into 6 micron sections, and placed on microscope slides. After fixation in cold acetone, the sections were dried at room temperature, then washed with phosphate buffered saline and blocked. The slides were incubated with antiserum against UT116 synthetic peptide, SEQUENCE ID NO 27 (at a dilution of 1 to 300); washed, incubated with biotinylated goat anti-rabbit antibody, washed again, and incubated with avidin labeled with horse radish peroxidase. After a final wash, the slides were incubated with 3-amino-9-ethylcarbazole substrate which gives a red stain. The slides were counterstained with hematoxylin, mounted, and examined under a microscope by a pathologist.

Anti-UT116 antibody showed moderate cytoplasmic immunoreactivity in the epithelium of all prostate specimens (benign and malignant) and intense cytoplasmic immunoreactivity in urothelium (benign and malignant). Breast epithelium also showed moderate to intense cytoplasmic immunoreactivity.

Results of all tissues examined are tabulated in Table 3. The column labeled "# pos" reports the number of specimens positive out of the total number of specimens examined. The column labeled "%" reports the average percent of cells which are positive.

Table 3. Tissue Staining by Anti-UT116 Antisera

TISSUE	# POS	%	COMMENTS
Colon, normal	2/4	30	Weak and equivocal immunoreactivity only on superficial cells
Colon, cancer	3/3	37	Weak and equivocal immunoreactivity
Lung, normal	0/4	0	
Lung, bronchial epithelium	0/4	0	Weak immunoreactivity on bronchial epithelium and on some intra-alveolar macrophages
Liver, normal hepatocytes	0/2	0	Intracytoplasmic background
Liver, normal bile duct epithelium	0/2	0	
Bladder, normal epithelium	5/5	90	Strong, cytoplasmic immunoreactivity; more intense on the superficial cells
Bladder, normal wall	0/7	0	Smooth muscle cells negative
Bladder cancer	1/1	90	Intense, cytoplasmic immunoreactivity
Breast, fibrocystic changes	1/1	80	Weak, epithelial immunoreactivity
Prostate, benign	14/14	49	Moderate background in the stroma
Prostate, cancer	15/15	64	Moderate and weak intensity in some cases
Breast, benign tissue	2/2	90	Moderate immunoreactivity

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## (1) GENERAL INFORMATION

(ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL  
FOR DETECTING DISEASES OF THE URINARY TRACT

(iii) NUMBER OF SEQUENCES: 31

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Abbott Laboratories
- (B) STREET: 100 Abbott Park Road
- (C) CITY: Abbott Park
- (D) STATE: IL
- (E) COUNTRY: USA
- (F) ZIP: 60064-3500

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/856,652
- (B) FILING DATE: 15-MAY-1997

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Becker, Cheryl L.
- (B) REGISTRATION NUMBER: 35,441
- (C) REFERENCE/DOCKET NUMBER: 6106.US.P1

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 847/935-1729
- (B) TELEFAX: 847/938-2623
- (C) TELEX:



(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 31
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 232
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 275
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 284
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CATTTGAGGC	CATATAAAGT	CACCTGAGGC	NCTCTCCACC	ACAGCCCACC	AGTGACCATG	60
AAGGCTGTGC	TGCTTGCCCT	GTTGATGGCA	GGCTTGGCCC	TGCAGCCAGG	CACTGCCCTG	120
CTGTGCTACT	CCTGCAAAGC	CCAGGTGAGC	AACGAGGACT	GCCTGCAGGT	GGAGAACTGC	180
ACCCAGCTGG	GGGAGCAGTG	CTGGACCGCG	CGCATCCGCG	CAGTTGGCCT	CNTGACCGTC	240
ATCAGCAAAG	CTGCAGCTTG	AACTGCGTGG	ATGANTCACA	GGANTACTAC		290

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAGGCCCTCT	CCACCACAGC	CCACCAGTGA	CCATGAAGGC	TGTGCTGCTT	GCCCTGTTGA	60
TGGCAGGCTT	GGCCCTGCAG	CCAGGCACTG	CCCTGCTGTG	CTACTCCTGC	AAAGCCCAGG	120
TGAGCAACGA	GGACTGCCTG	CAGGTGGAGA	ACTGCACCCA	GCTGGGGGAG	CAGTGCTGGA	180
CCGCGCGCAT	CCGCGCAGTT	GGCCTCCTGA	CCGTCAATCAG	CAAAGGCTGC	AGCTTGAAGT	240
GCGTGATGA	CTCACAGGAC	TACTACGTGG	GCAAGAAGAA	CATCACGTGC	TGT	293

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAGTGACCAT	GAAGGCTGTG	CTGCTTGCCC	TGTTGATGGC	AGGCTTGGCC	CTGCAGCCAG	60
GCACTGCCCT	GCTGTGCTAC	TCCTGCAAAG	CCCAGGTGAG	CAACGAGGAC	TGCCTGCAGG	120
TGGAGAACTG	CACCCAGCTG	GGGGAGCAGT	GCTGGACCGC	GCGCATCCGC	GCAGTTGGCC	180
TCCTGACCGT	CATCAGCAAA	GGCTGCAGCT	TGAACTGCGT	GGATGACTCA	CAGGACTACT	240
ACGTGGGCAA	GAAGAACATC	ACGTGCTGTG	ACACCGACT			279

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTGACCATGA	AGGCTGTGCT	GCTTGCCCTG	TTGATGGCAG	GCTTGGCCCT	GCAGCCAGGC	60
ACTGCCCTGC	TGTGCTACTC	CTGCAAAGCC	CAGGTGAGCA	ACGAGGACTG	CCTGCAGGTG	120
GAGAACTGCA	CCCAGCTGGG	GGAGCAGTGC	TGGACCGCGC	GCATCCGCGC	AGTTGGCCTC	180
CTGACCGTCA	TCAGCAAAGG	CTGCAGC				207

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGAGGACTGC	CTGCAGGTGG	AGAACTGCAC	CCAGCTGGGG	GAGCAGTGCT	GGACCGCGCG	60
CATCCGCGCA	GTTGGCCTCC	TGACCGTCAT	CAGCAAAGGC	TGCAGCTTGA	ACTGCGTGGA	120
TGACTCACAG	GACTACTACG	TGGGCAAGAA	GAACATCACG	TGCTGTGACA	CCGACTTGTG	180
CAACGCCAGC	GGGGCCCATG	CCCTGCAGCC	GGCTGCCGCC	ATCCTTGCGC	TGCTCCCTGC	240
ACTCGGCCTG	CTGCTCTGGG	GACCC				265

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTGCTGTGAC	ACCGACTTGT	GCAACGCCAG	CGGGGCCCCAT	GCCCTGCAGC	CGGCTGCCGC	60
CATCCTTGCG	CTGCTCCCTG	CACTCGGCCT	GCTGCTCTGG	GGACCCGGCC	AGCTATAGGC	120
TCTGGGGGGC	CCCGCTGCAG	CCCACACTGG	GTGTGGTGCC	CCAGGCCTCT	GTGCCACTCC	180
TCACAGACCT	GGCCAGTGG	GAGCCTGTCC	TGGTTCCTGA	GGCACATCCT		230

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ix) FEATURE:  
 (A) NAME/KEY: base\_polymorphism  
 (B) LOCATION: 70  
 (D) OTHER INFORMATION: /note= "'N' represents an A or G or  
 T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTGGCCCCAGT	GGGAGCCTGT	CCTGGTTCCT	GAGGCACATC	CTAACGCAAG	TCTGACCATG	60
TATGTCTGCN	CCCCTGTCCC	CCACCCTGAC	CCTCCCATGG	CCCTCTCCAG	GACTIONCCACC	120
CGGCAGATCA	GCTCTAGTGA	CACAGATCCG	CCTGCAGATG	GCCCCCTCAA	CCCTCTCTGC	180
TGCTGTTTCC	ATGGCCCAGC	ATTCTCCACC	CTTAACCCCTG	TGCTCAGGCA	CCT	233

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism  
 (B) LOCATION: 60  
 (D) OTHER INFORMATION: /note= "'N' represents an A or G or  
 T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCCTGGTTC	CTGAGGCACA	TCCTAACGCA	AGTCTGACCA	TGTATGTCTG	CACCCCTGTN	60
CCCCACCCTG	ACCCTCCCAT	GGCCCTCTCC	AGGACTCCCA	CCCGGCAGAT	CAGCTCTAGT	120
GACACAGATC	CGCCTGCAGA	TGGCCCCCTC	AACCCTCTCT	GCTGCTGTTT	CCATGGCCCCA	180
GCAATTCTCCA	CCCTTAACCC	TGTGCTCAGG	CACCTCTTCC	CCCAGGAAGC	CTTCCCTGCC	240
CACCCCATCT						250

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TAACCCTGTG	CTCAGGCACC	TCTTCCCCCA	GGAAGCCTTC	CCTGCCCCACC	CCATCTATGA	60
CTTGAGCCAG	GTCTGGTCCG	TGGTGTCCCC	CGCACCCAGC	AGGGGACAGG	CACTCAGGAG	120
GGCCCAGTAA	AGGCTGAGAT	GAAGTGGACT	GAGTAGAACT	GGAGGACAAG	AGTCGACGTG	180
AGTTCCTGGG	AGTCTCCAGA	GATGGGGCCT	GGAGGCCTGG	AGGAAGGGGC	CAGGCCTCAC	240
ATTCGTGGGG	CTCCCTGAA					259

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCTATGACT	TGAGCCAGGT	CTGGTCCGTG	GTGTCCCCCG	CACCCAGCAG	GGGACAGGCA	60
CTCAGGAGGG	CCCAGTAAAG	GCTGAGATGA	AGTGGACTGA	GAGAACTGG	AGGACAAGAG	120

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TCGACGTGAG	TTCCTGGGAG	TCTCCAGAGA	TGGGGCCTGG	AGGCCTGGAG	GAAGGGGCCA	180
GGCCTCACAT	TCGTGGGGCT	CCCTGAATGG	CAGCCTGAGC	ACAGCGTAGG	CCCTTAATAA	240
ACACCTGTTG	GAT					253

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTGACCATGA	AGGCTGTGCT	GCTTGCCCTG	TTGATGGCAG	GCTTGGCCCT	GCAGCCAGGC	60
ACTGCCCTGC	TGTGCTACTC	CTGCAAAGCC	CAGGTGAGCA	ACGAGGACTG	CCTGCAGGTG	120
GAGAACTGCA	CCCAGCTGGG	GGAGCAGTGC	TGGACCGCGC	GCATCCGCGC	AGTTGGCCTC	180
CTGACCGTCA	TCAGCAAAGG	CTGCAGCTTG	AACTGCGTGG	ATGACTCACA	GGACTACTAC	240
GTGGGCAAGA	AGAACATCAC	GTGCTGTGAC	ACCGACTTGT	GCAACGCCAG	CGGGGGCCAT	300
GCCCTGCAGC	CGGCTGCCGC	CATCCTTGCG	CTGCTCCCTG	CACTCGGCCT	GCTGCTCTGG	360
GGACCCGGCC	AGCTATAGGC	TCTGGGGGGC	CCCGCTGCAG	CCCACACTGG	GTGTGGTGCC	420
CCAGGCCTCT	GTGCCACTCC	TCACAGACCT	GGCCCAGTGG	GAGCCTGTCC	TGGTTCCTGA	480
GGCACATCCT	AACGCAAGTC	TGACCATGTA	TGTCTGCACC	CCTGTCCCCC	ACCCTGACCC	540
TCCCATGGCC	CTCTCCAGGA	CTCCCACCCG	GCAGATCAGC	TCTAGTGACA	CAGATCCGCC	600
TGCAGATGGC	CCCTCCAACC	CTCTCTGCTG	CTGTTTCCAT	GGCCCAGCAT	TCTCCACCCT	660
TAACCTGTG	CTCAGGCACC	TCTTCCCCCA	GGAAGCCTTC	CCTGCCCCAC	CCATCTATGA	720
CTTGAGCCAG	GTCTGGTCCG	TGGTGTCCCC	CGCACCCAGC	AGGGGACAGG	CACTCAGGAG	780
GGCCCAGTAA	AGGCTGAGAT	GAAGTGGACT	GAGTAGAACT	GGAGGACAAG	AGTCGACGTG	840
AGTTCCCTGG	AGTCTCCAGA	GATGGGGCCT	GGAGGCCTGG	AGGAAGGGGC	CAGGCCTCAC	900
ATTCGTGGGG	CTCCCTGAAT	GGCAGCCTGA	GCACAGCGTA	GGCCCTTAAT	AAACACCTGT	960
TGGATAAGCC	CA					972

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1023 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CATTTGAGGC	CATATAAAGT	CACCTGAGGC	CCTCTCCACC	ACAGCCCACC	AGTGACCATG	60
AAGGCTGTGC	TGCTTGCCCT	GTTGATGGCA	GGCTTGCCCC	TGCAGCCAGG	CACTGCCCTG	120
CTGTGCTACT	CCTGCAAAGC	CCAGGTGAGC	AACGAGGACT	GCCTGCAGGT	GGAGAACTGC	180
ACCCAGCTGG	GGGAGCAGTG	CTGGACCGCG	CGCATCCGCG	CAGTTGGCCT	CCTGACCGTC	240
ATCAGCAAAG	GCTGCAGCTT	GAAGTGCCTG	GATGACTCAC	AGGACTACTA	CGTGGGCAAG	300
AAGAACATCA	CGTGCTGTGA	CACCGACTTG	TGCAACGCCA	GCGGGGCCCA	TGCCCTGCAG	360
CCGGCTGCCG	CCATCCTTGC	GCTGCTCCCT	GCACTCGGCC	TGCTGCTCTG	GGGACCCGGC	420
CAGCTATAGG	CTCTGGGGGG	CCCCGCTGCA	GCCCACACTG	GGTGTGGTGC	CCCAGGCCTC	480
TGTGCCACTC	CTCACAGACC	TGGCCCAGTG	GGAGCCTGTC	CTGGTTCCTG	AGGCACATCC	540
TAACGCAAGT	CTGACCATGT	ATGTCTGCAC	CCCTGTCCCC	CACCCTGACC	CTCCCATGGC	600
CCTCTCCAGG	ACTCCCACCC	GGCAGATCAG	CTCTAGTGAC	ACAGATCCGC	CTGCAGATGG	660
CCCCTCCAAC	CCTCTCTGCT	GCTGTTTCCA	TGGCCCAGCA	TTCTCCACCC	TTAACCTGT	720
GCTCAGGCAC	CTCTTCCCCC	AGGAAGCCTT	CCCTGCCCCC	CCCATCTATG	ACTTGAGCCA	780
GGTCTGGTCC	GTGGTGTCCC	CCGCACCCAG	CAGGGGACAG	GCACTCAGGA	GGGCCCAGTA	840
AAGGTGAGA	TGAAGTGGAC	TGAGTAGAAC	TGGAGGACAA	GAGTCGACGT	GAGTTCCTGG	900
GAGTCTCCAG	AGATGGGGCC	TGGAGGCCTG	GAGGAAGGGG	CCAGGCCTCA	CATTCGTGGG	960
GCTCCCTGAA	TGGCAGCCTG	AGCACAGCGT	AGGCCCTTAA	TAAACACCTG	TTGATAAGC	1020
CCA						1023

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

(2) INFORMATION FOR SEQ ID NO:14:

(A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

AATTAATTCC CGGGTCGACG AGCTCACTAG TCGGCGGCCG CTCTAGAGGA TCCAAGCTCG 60  
GAATTCGG 68

(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

AGCGGATAAC AATTCACAC AGGA 24

(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

TGTAACACGA CGGCCAGT 18

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GTGGGCAAGA AGAACATCAC 20

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGCAAGTCTG ACCATGTATG TC

22

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCTGAGATGA AGTGGACTGA

20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CAGACCTGGC TCAAGTCATA G

21

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TAGGATGTGC CTCAGGAACC

20

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTCTTGCCCA CGTAGTAGTC

20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

04079874.06490  
065450"42862060

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TGACACCGAC TTGTGCAACG

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TCGACTCTTG TCCTCCAGTT CTACTC

26

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met	Lys	Ala	Val	Leu	Leu	Ala	Leu	Leu	Met	Ala	Gly	Leu	Ala	Leu	Gln
1				5					10					15	
Pro	Gly	Thr	Ala	Leu	Leu	Cys	Tyr	Ser	Cys	Lys	Ala	Gln	Val	Ser	Asn
			20					25					30		
Glu	Asp	Cys	Leu	Gln	Val	Glu	Asn	Cys	Thr	Gln	Leu	Gly	Glu	Gln	Cys
		35				40						45			
Trp	Thr	Ala	Arg	Ile	Arg	Ala	Val	Gly	Leu	Leu	Thr	Val	Ile	Ser	Lys
	50				55						60				
Gly	Cys	Ser	Leu	Asn	Cys	Val	Asp	Asp	Ser	Gln	Asp	Tyr	Tyr	Val	Gly
65				70						75				80	
Lys	Lys	Asn	Ile	Thr	Cys	Cys	Asp	Thr	Asp	Leu	Cys	Asn	Ala	Ser	Gly
			85						90					95	
Ala	His	Ala	Leu	Gln	Pro	Ala	Ala	Ala	Ile	Leu	Ala	Leu	Leu	Pro	Ala
			100					105						110	
Leu	Gly	Leu	Leu	Leu	Trp	Gly	Pro	Gly	Gln	Leu					
		115				120									

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala Gln Val Ser Asn Glu Asp  
1                  5                  10                  15  
Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys Trp Thr  
                20                  25                  30  
Ala Arg

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Arg 1	Ile	Arg	Ala 5	Val	Gly	Leu	Leu	Thr	Val 10	Ile	Ser	Lys	Gly	Cys 15	Ser
Leu	Asn	Cys	Val 20	Asp	Asp	Ser	Gln	Asp 25	Tyr	Tyr	Val	Gly	Lys 30	Lys	Asn
Ile	Thr	Cys 35	Cys	Asp	Thr	Asp	Leu 40	Cys							

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly Lys Lys Asn Ile Thr  
1 5 10 15  
Cys Cys Asp Thr Asp Leu Cys Asn Ala Ser Gly Ala His Ala  
20 25 30

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Leu Gln Pro Ala Ala Ala Ile Leu Ala Leu Leu Pro Ala Leu Gly Leu  
1 5 10 15  
Leu Leu Trp Gly Pro Gly Gln Leu  
20

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Asp Tyr Lys Asp Asp Asp Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Met His Thr Glu His  
1 5 10 15  
His His His His His  
20

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We Claim:

1. A method of detecting the presence of a target UT116 polynucleotide in a test sample, said method comprising:
- 5 (a) contacting the test sample with at least one UT116-specific polynucleotide or complement thereof; and
- (b) detecting the presence of said target UT116 polynucleotide in the test sample, wherein said UT116-specific polynucleotide has at least 50% identity with a polynucleotide selected from the group consisting of SEQUENCE ID NOS 1-12, and
- 10 fragments or complements thereof.
2. The method of claim 1, wherein said target UT116 polynucleotide is attached to a solid phase prior to performing step (a).
- 15 3. A method for detecting mRNA of UT116 in a test sample, comprising:
- (a) performing reverse transcription with at least one primer in order to produce cDNA;
- (b) amplifying the cDNA obtained from step (a) using UT116 oligonucleotides as sense and antisense primers to obtain UT116 amplicon; and
- 20 (c) detecting the presence of said UT116 amplicon, wherein the UT116 oligonucleotides utilized in steps (a) and (b) have at least 50% identity with a sequence selected from the group consisting of SEQUENCE ID NOS 1-12, and fragments or complements thereof.
- 25 4. The method of claim 3, wherein said test sample is reacted with a solid phase prior to performing one of steps (a), (b), or (c).
5. The method of claim 3, wherein said detection step comprises utilizing a detectable label capable of generating a measurable signal.
- 30 6. A method of detecting a target UT116 polynucleotide in a test sample suspected of containing said target, comprising:
- (a) contacting said test sample with at least one UT116 oligonucleotide as a sense primer and with at least one UT116 oligonucleotide as an anti-sense primer and
- 35 amplifying to obtain a first stage reaction product;
- (b) contacting said first stage reaction product with at least one other UT116 oligonucleotide to obtain a second stage reaction product, with the proviso that the

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other UT116 oligonucleotide is located 3' to the UT116 oligonucleotides utilized in step (a) and is complementary to said first stage reaction product; and

(c) detecting said second stage reaction product as an indication of the presence of the target UT116 polynucleotide, wherein the UT116 oligonucleotides utilized in steps (a) and (b) have at least 50% identity with a sequence selected from the group consisting of SEQUENCE ID NOS 1-12, and fragments or complements thereof.

7. The method of claim 6, wherein said test sample is reacted with a solid phase prior to performing one of steps (a), (b), or (c).

8. The method of claim 6, wherein said detection step comprises utilizing a detectable label capable of generating a measurable signal.

9. The method of claim 8, wherein said detectable label is reacted to a solid phase.

10. A method for producing a polypeptide comprising at least one UT116 epitope, said method comprising incubating host cells that have been transfected with an expression vector containing a polynucleotide sequence encoding a polypeptide, wherein said polypeptide comprises an amino acid sequence having at least 50% identity with an amino acid sequence selected from the group consisting of SEQUENCE ID NO 25, SEQUENCE ID NO 26, SEQUENCE ID NO 27, SEQUENCE ID NO 28 and SEQUENCE ID NO 29, and fragments thereof.

11. A method for detecting UT116 antigen in a test sample suspected of containing said UT116 antigen, comprising:

(a) contacting the test sample with an antibody or fragment thereof which specifically binds to at least one epitope of a UT116 antigen selected from the group consisting of SEQUENCE ID NO 25, SEQUENCE ID NO 26, SEQUENCE ID NO 27, SEQUENCE ID NO 28 and SEQUENCE ID NO 29, and fragments thereof, wherein said contacting is carried out for a time and under conditions sufficient for the formation of antibody/antigen complexes; and  
(b) detecting the presence of said complexes as an indication of the presence of said UT116 antigen..

12. The method of claim 11, wherein said antibody is attached to a solid phase.

13. A method for detecting the presence of antibodies specific for a UT116 antigen in a test sample suspected of containing such antibodies, said method comprising:

(a) contacting the test sample with a UT116 polypeptide, wherein said UT116 polypeptide contains at least one UT116 epitope derived from an amino acid sequence or fragment thereof having at least 50% identity to an amino acid sequence selected from the group consisting of SEQUENCE ID NO 25, SEQUENCE ID NO 26, SEQUENCE ID NO 27, SEQUENCE ID NO 28 and SEQUENCE ID NO 29, and fragments thereof, and further wherein said contacting is carried out for a time and under conditions sufficient to allow antigen/antibody complexes to form; and

(b) detecting the presence of said complexes as an indication of the presence of said antibodies specific for a UT116 antigen.

14. The method of claim 13, wherein said UT116 polypeptide is attached to a solid phase.

15. A method for producing antibodies which specifically bind to UT116 antigen, comprising administering to an individual an isolated immunogenic polypeptide or fragment thereof in an amount sufficient to elicit an immune response, wherein said immunogenic polypeptide comprises at least one UT116 epitope and has at least 50% identity to a sequence selected from the group consisting of SEQUENCE ID NO 25, SEQUENCE ID NO 26, SEQUENCE ID NO 27, SEQUENCE ID NO 28 and SEQUENCE ID NO 29, and fragments thereof.

16. A method for producing antibodies which specifically bind to UT116 antigen, comprising administering to an individual a plasmid comprising a sequence which encodes at least one UT116 epitope derived from a polypeptide having an amino acid sequence selected from the group consisting of SEQUENCE ID NO 25, SEQUENCE ID NO 26, SEQUENCE ID NO 27, SEQUENCE ID NO 28 and SEQUENCE ID NO 29, and fragments thereof.

17. The method of claim 1, wherein the presence of said target UT116 polynucleotide in said test sample is indicative of urinary tract disease.

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18. The method of claim 3, wherein the presence of said amplicon is indicative of urinary tract disease.

5 19. The method of claim 6, wherein the presence of said second stage reaction product is indicative of urinary tract disease.

20. The method of claim 11, wherein detection of said complexes is indicative of urinary tract disease.

10 21. The method of claim 13, wherein detection of said complexes is indicative of urinary tract disease.

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REAGENTS AND METHODS USEFUL FOR DETECTING  
DISEASES OF THE URINARY TRACT

5

Abstract of the Disclosure

10

A set of contiguous and partially overlapping cDNA sequences and polypeptides encoded thereby, designated as UT116 and transcribed from urinary tract tissue, is described. These sequences are useful for the detecting, diagnosing, staging, monitoring, prognosticating, in vivo imaging, preventing or treating, or determining the predisposition of an individual to diseases and conditions of the urinary tract, such as urinary tract cancer. Also provided are antibodies which specifically bind to UT116-  
15 encoded polypeptide or protein, and agonists or inhibitors which prevent action of the tissue-specific UT116 polypeptide, which molecules are useful for the therapeutic treatment of urinary tract diseases, tumors or metastases.

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# Figure 1A

>3353644	CATTTGAGGC	CATATAAAGT	CACCTGAGGC	NCTCTCCACC	ACAGCCCACC
>2804743			GAGGC	CCTCTCCACC	ACAGCCCACC
>1891065					C
Consensus	CATTTGAGGC	CATATAAAGT	CACCTGAGGC	CCTCTCCACC	ACAGCCCACC
>3353644	AGTGACCATG	AAGGCTGTGC	TGCTTGCCCT	GTTGATGGCA	GGCTTGGCCC
>2804743	AGTGACCATG	AAGGCTGTGC	TGCTTGCCCT	GTTGATGGCA	GGCTTGGCCC
>1891065	AGTGACCATG	AAGGCTGTGC	TGCTTGCCCT	GTTGATGGCA	GGCTTGGCCC
>1543671	GTGACCATG	AAGGCTGTGC	TGCTTGCCCT	GTTGATGGCA	GGCTTGGCCC
>1543671IH	GTGACCATG	AAGGCTGTGC	TGCTTGCCCT	GTTGATGGCA	GGCTTGGCCC
Consensus	AGTGACCATG	AAGGCTGTGC	TGCTTGCCCT	GTTGATGGCA	GGCTTGGCCC
>3353644	TGCAGCCAGG	CACTGCCCTG	CTGTGCTACT	CCTGCAAAGC	CCAGGTGAGC
>2804743	TGCAGCCAGG	CACTGCCCTG	CTGTGCTACT	CCTGCAAAGC	CCAGGTGAGC
>1891065	TGCAGCCAGG	CACTGCCCTG	CTGTGCTACT	CCTGCAAAGC	CCAGGTGAGC
>1543671	TGCAGCCAGG	CACTGCCCTG	CTGTGCTACT	CCTGCAAAGC	CCAGGTGAGC
>1543671IH	TGCAGCCAGG	CACTGCCCTG	CTGTGCTACT	CCTGCAAAGC	CCAGGTGAGC
Consensus	TGCAGCCAGG	CACTGCCCTG	CTGTGCTACT	CCTGCAAAGC	CCAGGTGAGC
>3353644	AACGAGGACT	GCCTGCAGGT	GGAGAACTGC	ACCCAGCTGG	GGGAGCAGTG
>2804743	AACGAGGACT	GCCTGCAGGT	GGAGAACTGC	ACCCAGCTGG	GGGAGCAGTG
>1891065	AACGAGGACT	GCCTGCAGGT	GGAGAACTGC	ACCCAGCTGG	GGGAGCAGTG
>1543671	AACGAGGACT	GCCTGCAGGT	GGAGAACTGC	ACCCAGCTGG	GGGAGCAGTG
>1543671IH	AACGAGGACT	GCCTGCAGGT	GGAGAACTGC	ACCCAGCTGG	GGGAGCAGTG
>1863905	CGAGGACT	GCCTGCAGGT	GGAGAACTGC	ACCCAGCTGG	GGGAGCAGTG
Consensus	AACGAGGACT	GCCTGCAGGT	GGAGAACTGC	ACCCAGCTGG	GGGAGCAGTG
>3353644	CTGGACCGCG	CGCATCCGCG	CAGTTGGCCT	CNTGACCGTC	ATCAGCAAAG
>2804743	CTGGACCGCG	CGCATCCGCG	CAGTTGGCCT	CCTGACCGTC	ATCAGCAAAG
>1891065	CTGGACCGCG	CGCATCCGCG	CAGTTGGCCT	CCTGACCGTC	ATCAGCAAAG
>1543671	CTGGACCGCG	CGCATCCGCG	CAGTTGGCCT	CC'TGACCGTC	ATCAGCAAAG
>1543671IH	CTGGACCGCG	CGCATCCGCG	CAGTTGGCCT	CCTGACCGTC	ATCAGCAAAG
>1863905	CTGGACCGCG	CGCATCCGCG	CAGTTGGCCT	CCTGACCGTC	ATCAGCAAAG
Consensus	CTGGACCGCG	CGCATCCGCG	CAGTTGGCCT	CC'TGACCGTC	ATCAGCAAAG
>3353644	:CTGCAGCTT	GAAGTGCCTG	GATGANTCAC	AGGANTACTA	C
>2804743	GCTGCAGCTT	GAAGTGCCTG	GATGACTCAC	AGGACTACTA	CGTGGGCAAG
>1891065	GCTGCAGCTT	GAAGTGCCTG	GATGACTCAC	AGGACTACTA	CGTGGGCAAG
>1543671	GCTGCAGC				
>1543671IH	GCTGCAGCTT	GAAGTGCCTG	GATGACTCAC	AGGACTACTA	CGTGGGCAAG
>1863905	GCTGCAGCTT	GAAGTGCCTG	GATGACTCAC	AGGACTACTA	CGTGGGCAAG
Consensus	GCTGCAGCTT	GAAGTGCCTG	GATGACTCAC	AGGACTACTA	CGTGGGCAAG
>2804743	AAGAACATCA	CGTGCTGTG			
>1891065	AAGAACATCA	CGTGCTGTGA	CACCGACTT		
>1543671IH	AAGAACATCA	CGTGCTGTGA	CACCGACTTG	TGCAACGCCA	GCGGGGCCCA
>1863905	AAGAACATCA	CGTGCTGTGA	CACCGACTTG	TGCAACGCCA	GCGGGGCCCA
>1314679		GTGCTGTGA	CACCGACTTG	TGCAACGCCA	GCGGGGCCCA
Consensus	AAGAACATCA	CGTGCTGTGA	CACCGACTTG	TGCAACGCCA	GCGGGGCCCA

## Figure 1B

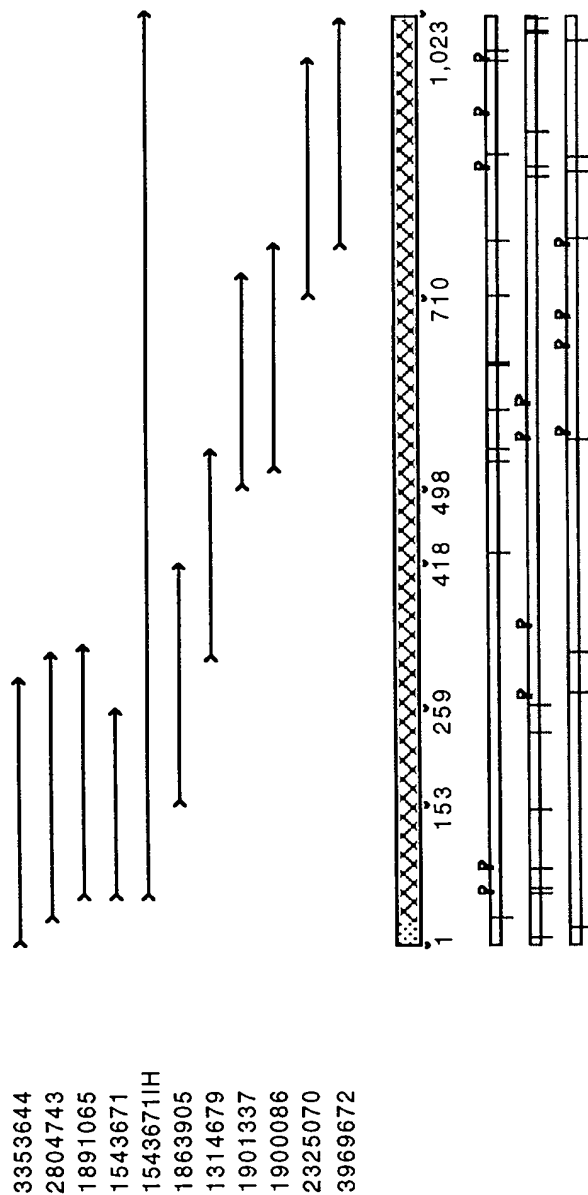
>1543671IH	TGCCCTGCAG	CCGGCTGCCG	CCATCCTTGC	GCTGCTCCCT	GCACTCGGCC
>1863905	TGCCCTGCAG	CCGGCTGCCG	CCATCCTTGC	GCTGCTCCCT	GCACTCGGCC
>1314679	TGCCCTGCAG	CCGGCTGCCG	CCATCCTTGC	GCTGCTCCCT	GCACTCGGCC
Consensus	TGCCCTGCAG	CCGGCTGCCG	CCATCCTTGC	GCTGCTCCCT	GCACTCGGCC
>1543671IH	TGCTGCTCTG	GGGACCCGGC	CAGCTATAGG	CTCTGGGGGG	CCCCGCTGCA
>1863905	TGCTGCTCTG	GGGACCC			
>1314679	TGCTGCTCTG	GGGACCCGGC	CAGCTATAGG	CTCTGGGGGG	CCCCGCTGCA
Consensus	TGCTGCTCTG	GGGACCCGGC	CAGCTATAGG	CTCTGGGGGG	CCCCGCTGCA
>1543671IH	GCCCACACTG	GGTGTGGTGC	CCCAGGCCTC	TGTGCCACTC	CTCACAGACC
>1314679	GCCCACACTG	GGTGTGGTGC	CCCAGGCCTC	TGTGCCACTC	CTCACAGACC
>1901337					C
Consensus	GCCCACACTG	GGTGTGGTGC	CCCAGGCCTC	TGTGCCACTC	CTCACAGACC
>1543671IH	TGGCCCAAGT	GGAGCCTGTC	CTGGTTCCTG	AGGCACATCC	TAACGCAAGT
>1314679	TGGCCCAAGT	GGAGCCTGTC	CTGGTTCCTG	AGGCACATCC	T
>1901337	TGGCCCAAGT	GGAGCCTGTC	CTGGTTCCTG	AGGCACATCC	TAACGCAAGT
>1900086		GTC	CTGGTTCCTG	AGGCACATCC	TAACGCAAGT
Consensus	TGGCCCAAGT	GGAGCCTGTC	CTGGTTCCTG	AGGCACATCC	TAACGCAAGT
>1543671IH	CTGACCATGT	ATGTCTGCAC	CCCTGTCCCC	CACCCTGACC	CTCCCATGGC
>1901337	CTGACCATGT	ATGTCTGCNC	CCCTGTCCCC	CACCCTGACC	CTCCCATGGC
>1900086	CTGACCATGT	ATGTCTGCAC	CCCTGTNCCC	CACCCTGACC	CTCCCATGGC
Consensus	CTGACCATGT	ATGTCTGCAC	CCCTGTCCCC	CACCCTGACC	CTCCCATGGC
>1543671IH	CCTCTCCAGG	ACTCCCACCC	GGCAGATCAG	CTCTAGTGAC	ACAGATCCGC
>1901337	CCTCTCCAGG	ACTCCCACCC	GGCAGATCAG	CTCTAGTGAC	ACAGATCCGC
>1900086	CCTCTCCAGG	ACTCCCACCC	GGCAGATCAG	CTCTAGTGAC	ACAGATCCGC
Consensus	CCTCTCCAGG	ACTCCCACCC	GGCAGATCAG	CTCTAGTGAC	ACAGATCCGC
>1543671IH	CTGCAGATGG	CCCCTCCAAC	CCTCTCTGCT	GCTGTTTCCA	TGGCCCAGCA
>1901337	CTGCAGATGG	CCCCTCCAAC	CCTCTCTGCT	GCTGTTTCCA	TGGCCCAGCA
>1900086	CTGCAGATGG	CCCCTCCAAC	CCTCTCTGCT	GCTGTTTCCA	TGGCCCAGCA
Consensus	CTGCAGATGG	CCCCTCCAAC	CCTCTCTGCT	GCTGTTTCCA	TGGCCCAGCA
>1543671IH	TTCTCCACCC	TTAACCCTGT	GCTCAGGCAC	CTCTTCCCCC	AGGAAGCCTT
>1901337	TTCTCCACCC	TTAACCCTGT	GCTCAGGCAC	CT	
>1900086	TTCTCCACCC	TTAACCCTGT	GCTCAGGCAC	CTCTTCCCCC	AGGAAGCCTT
>2325070		TAACCCTGT	GCTCAGGCAC	CTCTTCCCCC	AGGAAGCCTT
Consensus	TTCTCCACCC	TTAACCCTGT	GCTCAGGCAC	CTCTTCCCCC	AGGAAGCCTT
>1543671IH	CCCTGCCCCAC	CCCATCTATG	ACTTGAGCCA	GGTCTGGTCC	GTGGTGTCCC
>1900086	CCCTGCCCCAC	CCCATCT			
>2325070	CCCTGCCCCAC	CCCATCTATG	ACTTGAGCCA	GGTCTGGTCC	GTGGTGTCCC
>3969672		ATCTATG	ACTTGAGCCA	GGTCTGGTCC	GTGGTGTCCC
Consensus	CCCTGCCCCAC	CCCATCTATG	ACTTGAGCCA	GGTCTGGTCC	GTGGTGTCCC
>1543671IH	CCGCACCCAG	CAGGGGACAG	GCACTCAGGA	GGGCCCAGTA	AAGGCTGAGA
>2325070	CCGCACCCAG	CAGGGGACAG	GCACTCAGGA	GGGCCCAGTA	AAGGCTGAGA
>3969672	CCGCACCCAG	CAGGGGACAG	GCACTCAGGA	GGGCCCAGTA	AAGGCTGAGA
Consensus	CCGCACCCAG	CAGGGGACAG	GCACTCAGGA	GGGCCCAGTA	AAGGCTGAGA



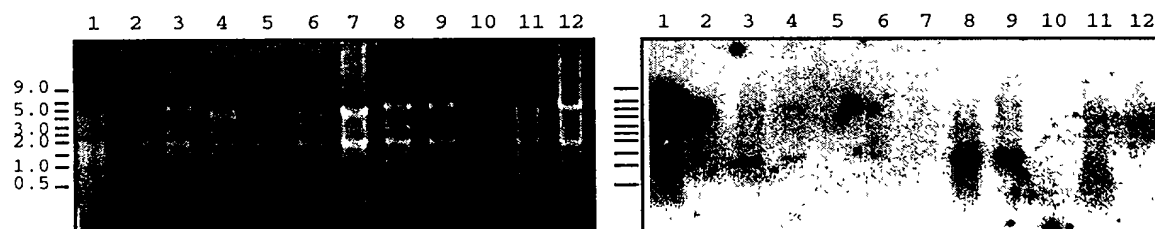
## Figure 1C

>1543671IH	TGAAGTGGAC	TGAGTAGAAC	TGGAGGACAA	GAGTCGACGT	GAGTTCCTGG
>2325070	TGAAGTGGAC	TGAGTAGAAC	TGGAGGACAA	GAGTCGACGT	GAGTTCCTGG
>3969672	TGAAGTGGAC	TGAGTAGAAC	TGGAGGACAA	GAGTCGACGT	GAGTTCCTGG
Consensus	TGAAGTGGAC	TGAGTAGAAC	TGGAGGACAA	GAGTCGACGT	GAGTTCCTGG
>1543671IH	GAGTCTCCAG	AGATGGGGCC	TGGAGGCCTG	GAGGAAGGGG	CCAGGCCCTCA
>2325070	GAGTCTCCAG	AGATGGGGCC	TGGAGGCCTG	GAGGAAGGGG	CCAGGCCCTCA
>3969672	GAGTCTCCAG	AGATGGGGCC	TGGAGGCCTG	GAGGAAGGGG	CCAGGCCCTCA
Consensus	GAGTCTCCAG	AGATGGGGCC	TGGAGGCCTG	GAGGAAGGGG	CCAGGCCCTCA
>1543671IH	CATTCGTGGG	GCTCCCTGAA	TGGCAGCCTG	AGCACAGCGT	AGGCCCTTAA
>2325070	CATTCGTGGG	GCTCCCTGAA			
>3969672	CATTCGTGGG	GCTCCCTGAA	TGGCAGCCTG	AGCACAGCGT	AGGCCCTTAA
Consensus	CATTCGTGGG	GCTCCCTGAA	TGGCAGCCTG	AGCACAGCGT	AGGCCCTTAA
>1543671IH	TAAACACCTG	TTGGATAAGC	CCA		
>3969672	TAAACACCTG	TTGGAT			
Consensus	TAAACACCTG	TTGGATAAGC	CCA		

Figure 2



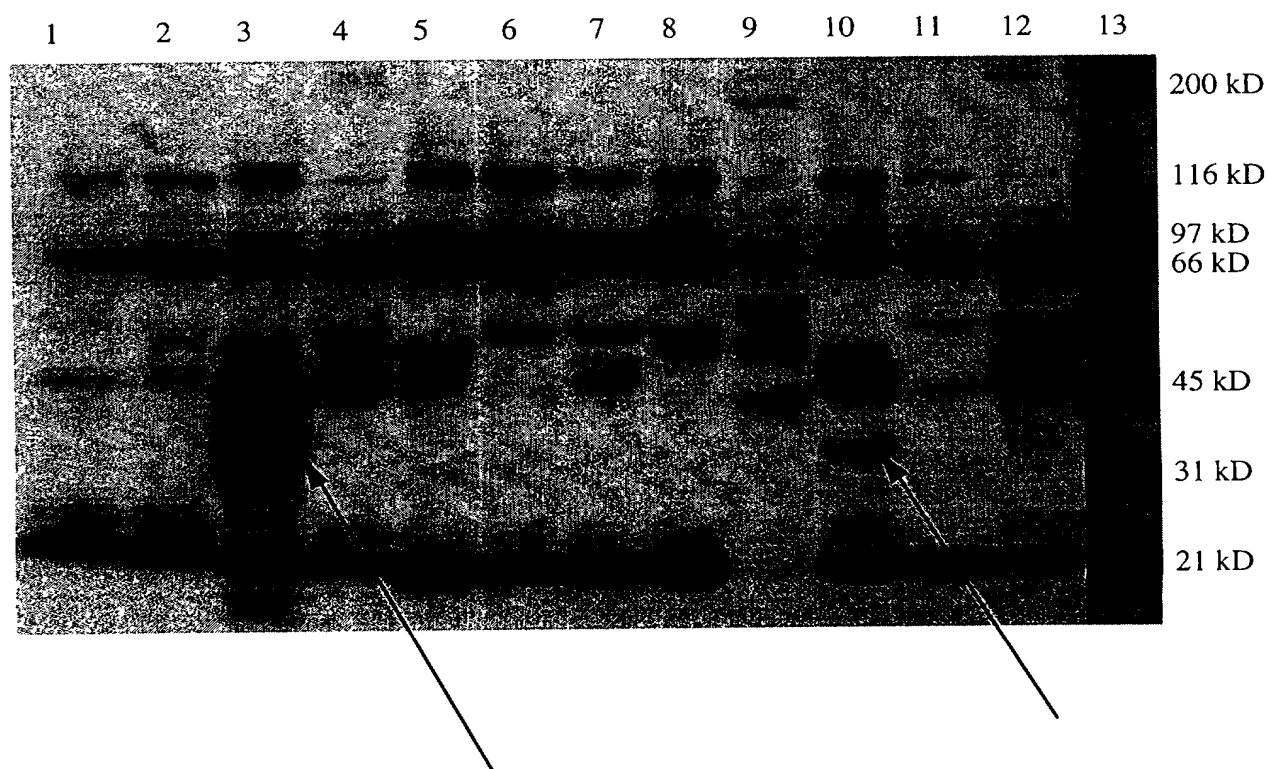
**Figure 3**



Lane	Tissue	Lane	Tissue
1	Normal Bladder	7	Bladder Cancer
2	Normal Bladder	8	Bladder Cancer
3	Normal Bladder	9	Bladder Cancer
4	Normal Bladder	10	Bladder Cancer
5	Normal Bladder	11	Bladder Cancer
6	Normal Bladder	12	PS116 Bacterial RNA

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**Figure 4**



Lane	Tissue	Lane	Tissue
1	Bladder Cancer	8	Breast
2	Bladder	9	Prostate Cancer
3	Bladder Cancer	10	Prostate Cancer
4	Bladder	11	Prostate Cancer
5	Bladder Cancer	12	BPH
6	Colon	13	Markers
7	Lung		

## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: Patricia A. BILLING-  
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Michael R. KLASS, Jon D. KRATOCHVIL,  
Lisa ROBERTS-RAPP, John C. RUSSELL  
and Stephen D. STROUPE

Serial No.: CIP of 08/856,652

Filed: on even date herewith

Title: REAGENTS AND METHODS  
USEFUL FOR DETECTING DISEASES OF  
THE URINARY TRACT

Case No.: 6106.US.P1

Certificate of Mailing Under 37 C.F.R. §1.10

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I hereby certify that this paper (along with any paper referred to as being attached or enclosed) is being deposited with the United States Postal Service on the date shown below as Express Mail Post Office to Addressee Service addressed to:

Assistant Commissioner for Patents  
**BOX PATENT APPLICATION**  
Washington, D.C. 20231  
on

May 15, 1998  
Date

Patricia K. Himenes  
Patricia K. Himenes

**DECLARATION AND POWER OF ATTORNEY FOR A UNITED STATES PATENT APPLICATION**

Assistant Commissioner for Patents

**Box Patent Application**

Washington, D.C. 20231

As a below-named inventor, I hereby declare that my residence, post office address and citizenship are as stated below next to my name. I believe that I am an original and first and joint inventor of the subject matter of the invention entitled REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF THE URINARY TRACT, which is claimed and for which a patent is sought in the patent application attached hereto.

I hereby state that I have reviewed and understand the contents of the above-mentioned specification, including the claims.

I acknowledge a duty to disclose to the Patent and Trademark Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56.

Claim to benefit of foreign application(s):

I hereby claim foreign priority benefits under 35 U.S.C. §119 for the following foreign application(s) for patent or inventor's certificate:

NONE

The following foreign applications for patent or inventor's certificate have a filing date earlier than the filing date of the application(s) identified above:

NONE

Claim to benefit of U.S. Application(s):

I hereby claim the benefit under 35 U.S.C. §120 of the following earlier-filed United States patent application(s):

U.S. Serial No. 08/856,652 filed May 15, 1997, pending.

Insofar as the subject matter of each of the claims of this/these application(s) is not disclosed in the prior U.S. Applications in the manner required by 35 U.S.C. § 112, first paragraph, I acknowledge a duty to disclose to the Patent and Trademark Office all information known to me to be material to patentability as defined in 37 C.F.R. Which came into existence between the filing date(s) of the prior applications and the national or PCT filing date of this application.

I hereby appoint the following Attorneys and/or agents to prosecute this application and any continuation or divisional applications based hereon, and to transact all business in the Patent and Trademark Office connected therewith:

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Citizenship: US

I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that all statements made herein were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Patricia A. BILLING-MEDEL

Maurice COHEN

Tracey L. COLPITTS

Paula N. FRIEDMAN

Edward N. GRANADOS

Steven C. HODGES

Michael R. KLASS

Jon D. KRATOCHVIL

Lisa ROBERTS-RAPP

John C. RUSSELL

Stephen D. STROUPE



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**PATENT APPLICATION US/09/079,874**

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**This Raw Listing contains the General Information Section and up to the first 5 pages.**

## SEQUENCE LISTING

(1) General Information

(i) APPLICANT: BILLING-MEDEL, PATRICIA  
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COLPITTS, TRACEY L.  
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GRANADOS, EDWARD N.  
HODGES, STEVEN C.  
KLASS, MICHAEL R.  
KRATOCHVIL, JON D.  
ROBERTS-RAPP, LISA  
RUSSELL, JOHN C.  
STROUPE, STEPHEN D.

ENTERED

(ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL  
FOR DETECTING DISEASES OF THE URINARY TRACT

(iii) NUMBER OF SEQUENCES: 31

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Abbott Laboratories  
(B) STREET: 100 Abbott Park Road  
(C) CITY: Abbott Park  
(D) STATE: IL  
(E) COUNTRY: USA  
(F) ZIP: 60064-3500

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

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48 (vii) PRIOR APPLICATION DATA:  
49 (A) APPLICATION NUMBER: 08/856,652  
50 (B) FILING DATE: 15-MAY-1997  
51  
52  
53  
54 (viii) ATTORNEY/AGENT INFORMATION:  
55 (A) NAME: Becker, Cheryl L.  
56 (B) REGISTRATION NUMBER: 35,441  
57 (C) REFERENCE/DOCKET NUMBER: 6106.US.P1  
58  
59 (ix) TELECOMMUNICATION INFORMATION:  
60 (A) TELEPHONE: 847/935-1729  
61 (B) TELEFAX: 847/938-2623  
62 (C) TELEX:  
63  
64  
65 (2) INFORMATION FOR SEQ ID NO:1:  
66  
67 (i) SEQUENCE CHARACTERISTICS:  
68 (A) LENGTH: 290 base pairs  
69 (B) TYPE: nucleic acid  
70 (C) STRANDEDNESS: single  
71 (D) TOPOLOGY: linear  
72  
73 (ix) FEATURE:  
74 (A) NAME/KEY: base\_polymorphism  
75 (B) LOCATION: 31  
76 (D) OTHER INFORMATION: /note= " N' represents an A or G or  
77 T or C polymorphism at this position"  
78  
79 (ix) FEATURE:  
80 (A) NAME/KEY: base\_polymorphism  
81 (B) LOCATION: 232  
82 (D) OTHER INFORMATION: /note= " N' represents an A or G or  
83 T or C polymorphism at this position"  
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85 (ix) FEATURE:  
86 (A) NAME/KEY: base\_polymorphism  
87 (B) LOCATION: 275  
88 (D) OTHER INFORMATION: /note= " N' represents an A or G or  
89 T or C polymorphism at this position"  
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91 (ix) FEATURE:  
92 (A) NAME/KEY: base\_polymorphism  
93 (B) LOCATION: 284  
94 (D) OTHER INFORMATION: /note= " N' represents an A or G or  
95 T or C polymorphism at this position"  
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98 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
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101	AAGGCTGTGC	TGCTTGCCCT	GTTGATGGCA	GGCTTGCCCC	TGCAGCCAGG	CACTGCCCTG	120
102	CTGTGCTACT	CCTGCAAAGC	CCAGGTGAGC	AACGAGGACT	GCCTGCAGGT	GGAGAACTGC	180
103	ACCCAGCTGG	GGGAGCAGTG	CTGGACC CGC	CGCATCCGCG	CAGTTGGCCT	CNTGACCGTC	240
104	ATCAGCAAAG	CTGCAGCTTG	AACTGCGTGG	ATGANTCACA	GGANTACTAC		290

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

117	GAGGCCCTCT	CCACCACAGC	CCACCAGTGA	CCATGAAGGC	TGTGCTGCTT	GCCCTGTTGA	60
118	TGGCAGGCTT	GGCCCTGCAG	CCAGGCACTG	CCCTGCTGTG	CTACTCCTGC	AAAGCCCAGG	120
119	TGAGCAACGA	GGACTGCCTG	CAGGTGGAGA	ACTGCACCCA	GCTGGGGGAG	CAGTGCTGGA	180
120	CCGCGCGCAT	CCGCGCAGTT	GGCCTCCTGA	CCGTATCAG	CAAAGGCTGC	AGCTTGAAC	240
121	GCGTGATGA	CTCACAGGAC	TACTACGTGG	GCAAGAAGAA	CATCACGTGC	TGT	293

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

134	CAGTGACCAT	GAAGGCTGTG	CTGCTTGCCC	TGTTGATGGC	AGGCTTGGCC	CTGCAGCCAG	60
135	GCACTGCCCT	GCTGTGCTAC	TCCTGCAAAG	CCCAGGTGAG	CAACGAGGAC	TGCCTGCAGG	120
136	TGGAGAACTG	CACCCAGCTG	GGGGAGCAGT	GCTGGACCGC	GCGCATCCGC	GCAGTTGGCC	180
137	TCCTGACCGT	CATCAGCAAA	GGCTGCAGCT	TGAACTGCGT	GGATGACTCA	CAGGACTACT	240
138	ACGTGGGCAA	GAAGAACATC	ACGTGCTGTG	ACACCGACT			279

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

151	GTGACCATGA	AGGCTGTGCT	GCTTGCCCTG	TTGATGGCAG	GCTTGCCCTT	GCAGCCAGGC	60
152	ACTGCCCTGC	TGTGCTACTC	CTGCAAAGCC	CAGGTGAGCA	ACGAGGACTG	CCTGCAGGTG	120

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153 GAGAACTGCA CCCAGCTGGG GGAGCAGTGC TGGACCGCGC GCATCCGCGC AGTTGGCCTC 180  
154 CTGACCGTCA TCAGCAAAGG CTGCAGC 207

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

167 CGAGGACTGC CTGCAGGTGG AGAACTGCAC CCAGCTGGGG GAGCAGTGCT GGACCGCGCG 60  
168 CATCCGCGCA GTTGGCCTCC TGACCGTCAT CAGCAAAGGC TGCAGCTTGA ACTGCGTGGA 120  
169 TGACTCACAG GACTACTACG TGGGCAAGAA GAACATCACG TGCTGTGACA CCGACTTGTG 180  
170 CAACGCCAGC GGGGCCCCATG CCCTGCAGCC GGCTGCCGCC ATCCTTGCGC TGCTCCCTGC 240  
171 ACTCGGCCTG CTGCTCTGGG GACCC 265

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

184 GTGCTGTGAC ACCGACTTGT GCAACGCCAG CGGGGCCCCAT GCCCTGCAGC CGGCTGCCGC 60  
185 CATCCTTGCG CTGCTCCCTG CACTCGGCCT GCTGCTCTGG GGACCCGGCC AGCTATAGGC 120  
186 TCTGGGGGGC CCCGCTGCAG CCCACACTGG GTGTGGTGCC CCAGGCCTCT GTGCCACTCC 180  
187 TCACAGACCT GGCCAGTGG GAGCCTGTCC TGGTTCCTGA GGCACATCCT 230

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism  
(B) LOCATION: 70  
(D) OTHER INFORMATION: /note= " N' represents an A or G or  
T or C polymorphism at this position"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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TIME: 08:25:24

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206	CTGGCCCAGT	GGGAGCCTGT	CCTGGTTCCT	GAGGCACATC	CTAACGCAAG	TCTGACCATG	60
207	TATGTCTGCN	CCCCGTGCCC	CCACCCCTGAC	CCTCCCATGG	CCCTCTCCAG	GA CTCCCACC	120
208	CGGCAGATCA	GCTCTAGTGA	CACAGATCCG	CCTGCAGATG	GCCCCCTCAA	CCCTCTCTGC	180
209	TGCTGTTTCC	ATGGCCCAGC	ATTCTCCACC	CTTAACCCTG	TGCTCAGGCA	CCT	233

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 60
- (D) OTHER INFORMATION: /note= " N' represents an A or G or T or C polymorphism at this position"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

226	GTCCTGGTTC	CTGAGGCACA	TCCTAACGCA	AGTCTGACCA	TGTATGTCTG	CACCCCTGTN	60
227	CCCCACCCTG	ACCCTCCCAT	GGCCCTCTCC	AGGACTCCCA	CCCGGCAGAT	CAGCTCTAGT	120
228	GACACAGATC	CGCCTGCAGA	TGGCCCTTCC	AACCTCTCT	GCTGCTGTTT	CCATGGCCCA	180
229	GCATTCTCCA	CCCTTAACCC	TGTGCTCAGG	CACCTCTTCC	CCCAGGAAGC	CTTCCCTGCC	240
230	CACCCCATCT						250

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

242	TAACCCTGTG	CTCAGGCACC	TCTTCCCCCA	GGAAGCCTTC	CCTGCCCACC	CCATCTATGA	60
243	CTTGAGCCAG	GTCTGGTCCG	TGGTGTCCCC	CGCACCCAGC	AGGGGACAGG	CACTCAGGAG	120
244	GGCCCAGTAA	AGGCTGAGAT	GAAGTGGACT	GAGTAGAACT	GGAGGACAAG	AGTCGACGTG	180
245	AGTTCTTGGG	AGTCTCCAGA	GATGGGGCCT	GGAGGCCTGG	AGGAAGGGGC	CAGGCCTCAC	240
246	ATTCGTGGGG	CTCCCTGAA					259

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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